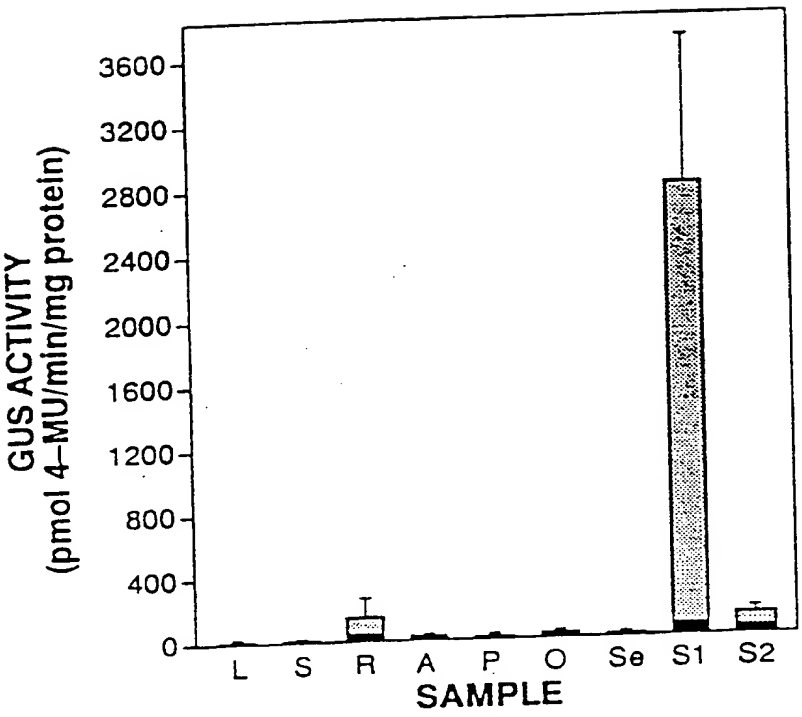

GUS ACTIVITY
(pmol 4-MU/min/mg protein)
3600
3200
2800
2400
2000
1600
1200
800
400
0
L
S
R
A
P
O
Se
S1
S2
SAMPLE

FIGURE 1

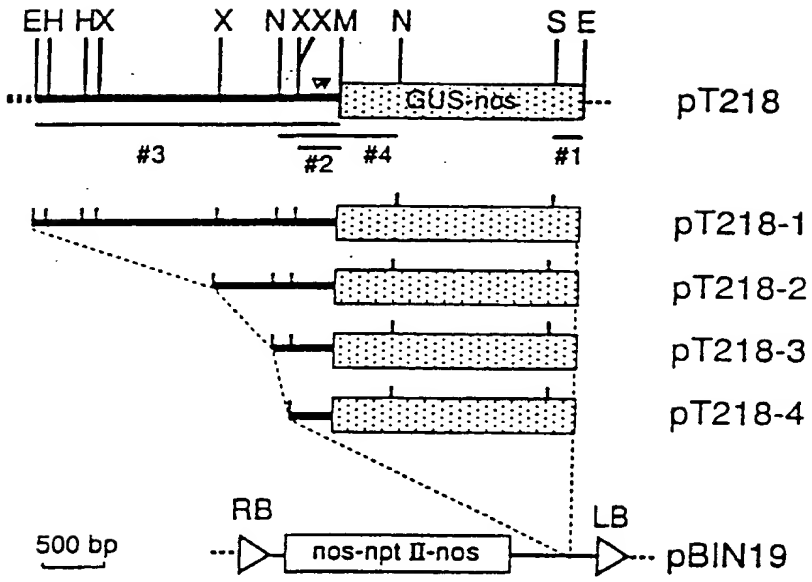

EH HX
X
N XXM
N
S E
GUS-nos
pT218
#3
#2
#4
#1
pT218-1
pT218-2
pT218-3
pT218-4
RB
LB
500 bp
nos-npt II-nos
pBIN19

FIGURE 2

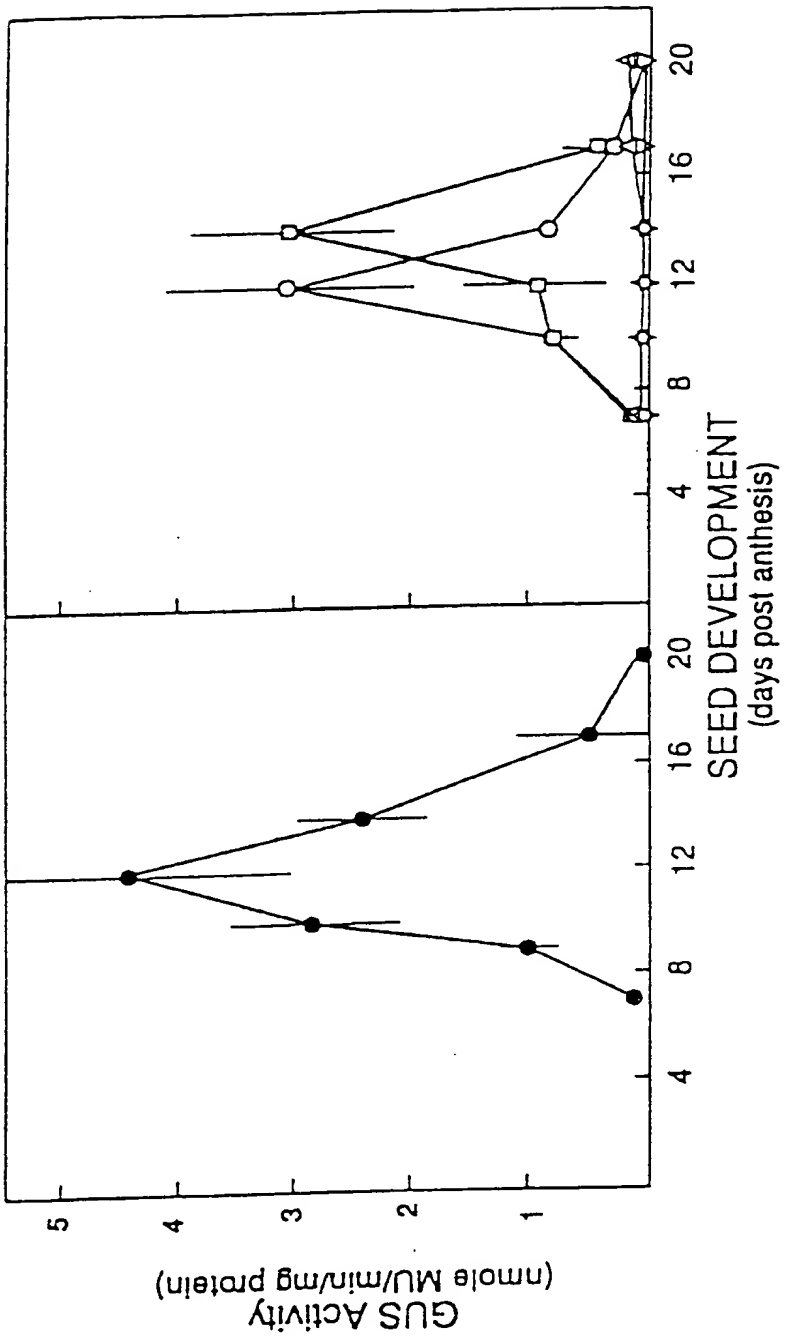

GUS Activity
(nmole MU/min/mg protein)
1
2
3
4
5
4
8
12
16
20
SEED DEVELOPMENT
(days post anthesis)
4
8
12
16
20

FIG. 3A

FIG. 3B

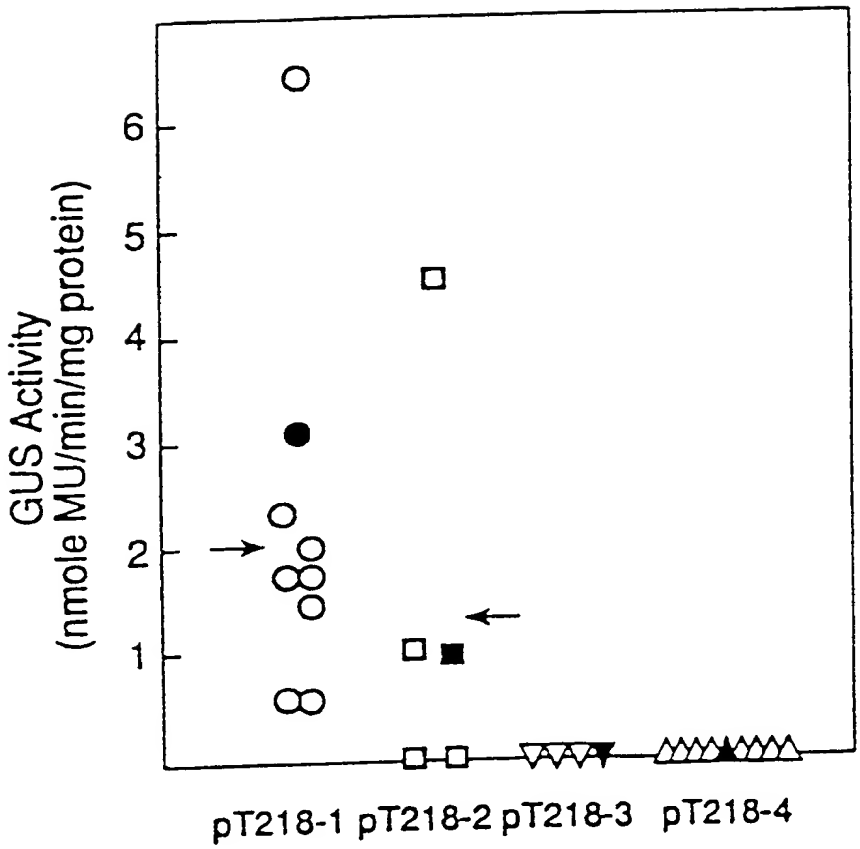

GUS Activity
(nmole MU/min/mg protein)
1
2
3
4
5
6
pT218-1
pT218-2
pT218-3
pT218-4

FIGURE 4

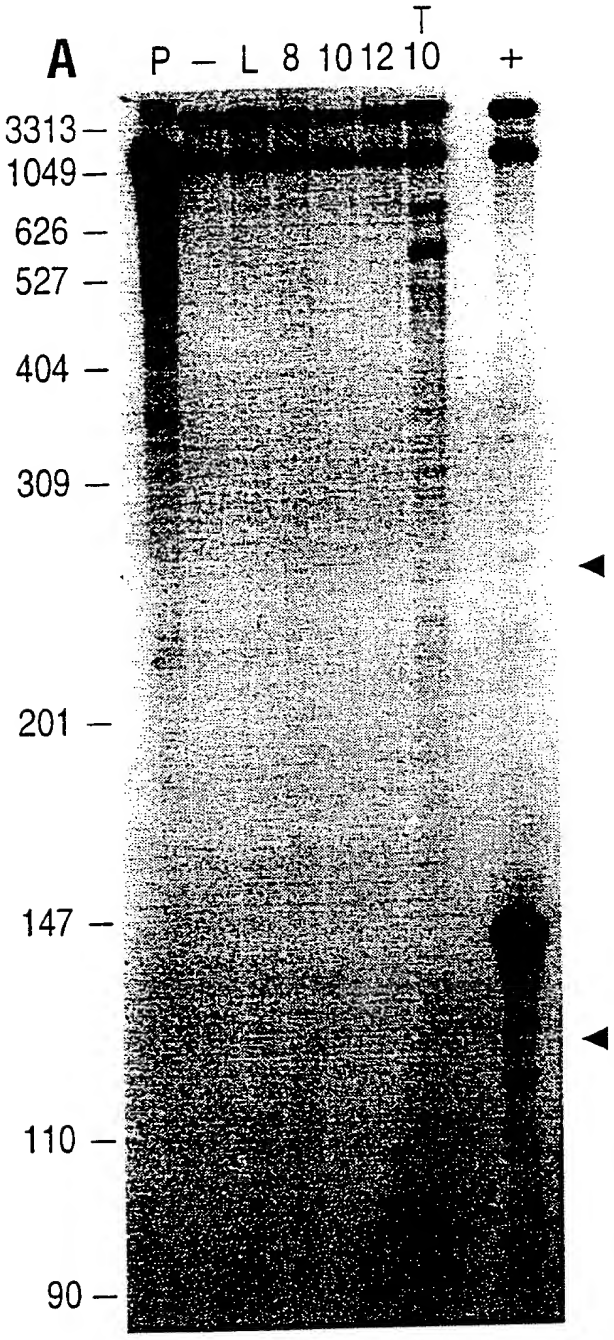

A
P – L 8 10 12 10 +
T
3313
1049
626
527
404
309
201
147
110
90

FIG. 5A

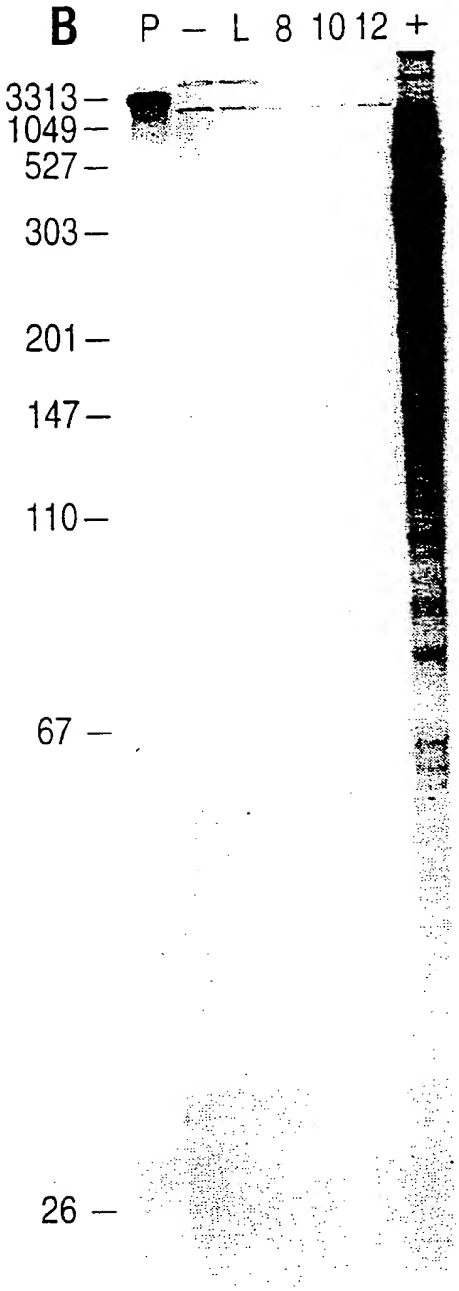

B
P – L 8 10 12 +
3313
1049
527
303
201
147
110
67
26

FIG. 5B

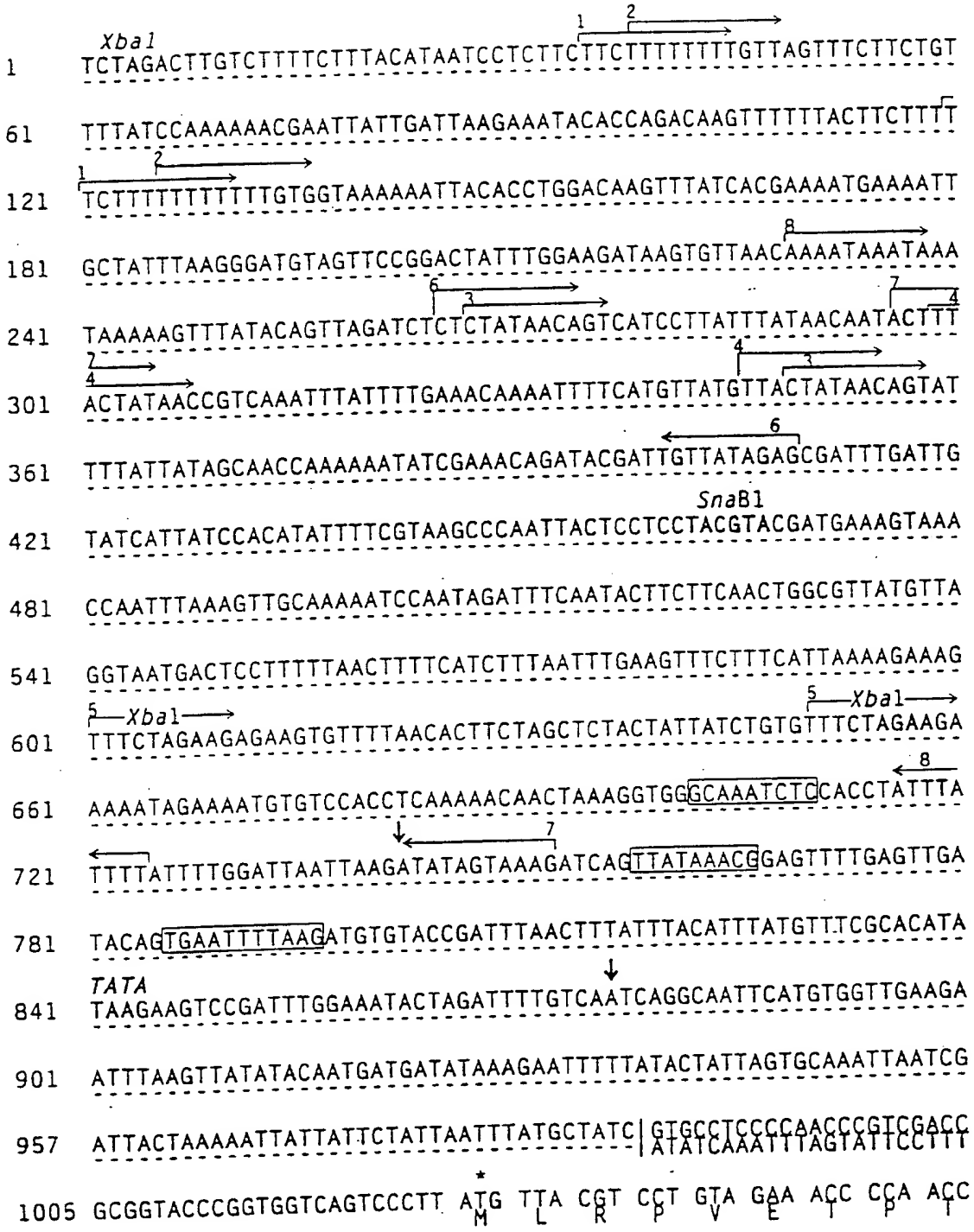

XbaI
1 TCTAGACTTGTCTTTTCTTTACATAATCCTCTTCTTCTTTTTTTTGTTAGTTTCTTCTGT
61 TTTATCCAAAAAACGAATTATTGATTAAGAAATACACCAGACAAGTTTTTTACTTCTTTT
121 TCTTTTTTTTTTTGTGGTAAAAAATTACACCTGGACAAGTTTATCACGAAAATGAAAATT
181 GCTATTTAAGGGATGTAGTTCCGGACTATTTGGAAGATAAGTGTTAACAAAATAAATAAA
241 TAAAAAGTTTATACAGTTAGATCTCTCTATAACAGTCATCCTTATTTATAACAATACTTT
301 ACTATAACCGTCAAATTTATTTTGAAACAAAATTTTCATGTTATGTTACTATAACAGTAT
361 TTTATTATAGCAACCAAAAAATATCGAAACAGATACGATTGTTATAGAGCGATTTGATTG
SnaB1
421 TATCATTATCCACATATTTTCGTAAGCCCAATTACTCCTCCTACGTACGATGAAAGTAAA
481 CCAATTTAAAGTTGCAAAAATCCAATAGATTTCAATACTTCTTCAACTGGCGTTATGTTA
541 GGTAATGACTCCTTTTTAACTTTTCATCTTTAATTTGAAGTTTCTTTCATTAAAAGAAAG
XbaI
601 TTTCTAGAAGAGAAGTGTTTTAACACTTCTAGCTCTACTATTATCTGTGTTTCTAGAAGA
661 AAAATAGAAAATGTGTCCACCTCAAAAACAACTAAAGGTGGGCAAATCTCCACCTATTTA
721 TTTTATTTTGGATTAATTAAGATATAGTAAAGATCAGTTATAAACGGAGTTTTGAGTTGA
781 TACAGTGAATTTTAAGATGTGTACCGATTTAACTTTATTTACATTTATGTTTCGCACATA
TATA
841 TAAGAAGTCCGATTTGGAAATACTAGATTTTGTCAATCAGGCAATTCATGTGGTTGAAGA
901 ATTTAAGTTATATACAATGATGATATAAAGAATTTTTATACTATTAGTGCAAATTAATCG
957 ATTACTAAAAATTATTATTCTATTAATTTATGCTATC|GTGCCTCCCCAACCCGTCGACC
ATATCAAATTTAGTATTCCTTT
1005 GCGGTACCCGGTGGTCAGTCCCTT ATG TTA CGT CCT GTA GAA ACC CCA ACC
M L R P V E T P T

FIGURE 6

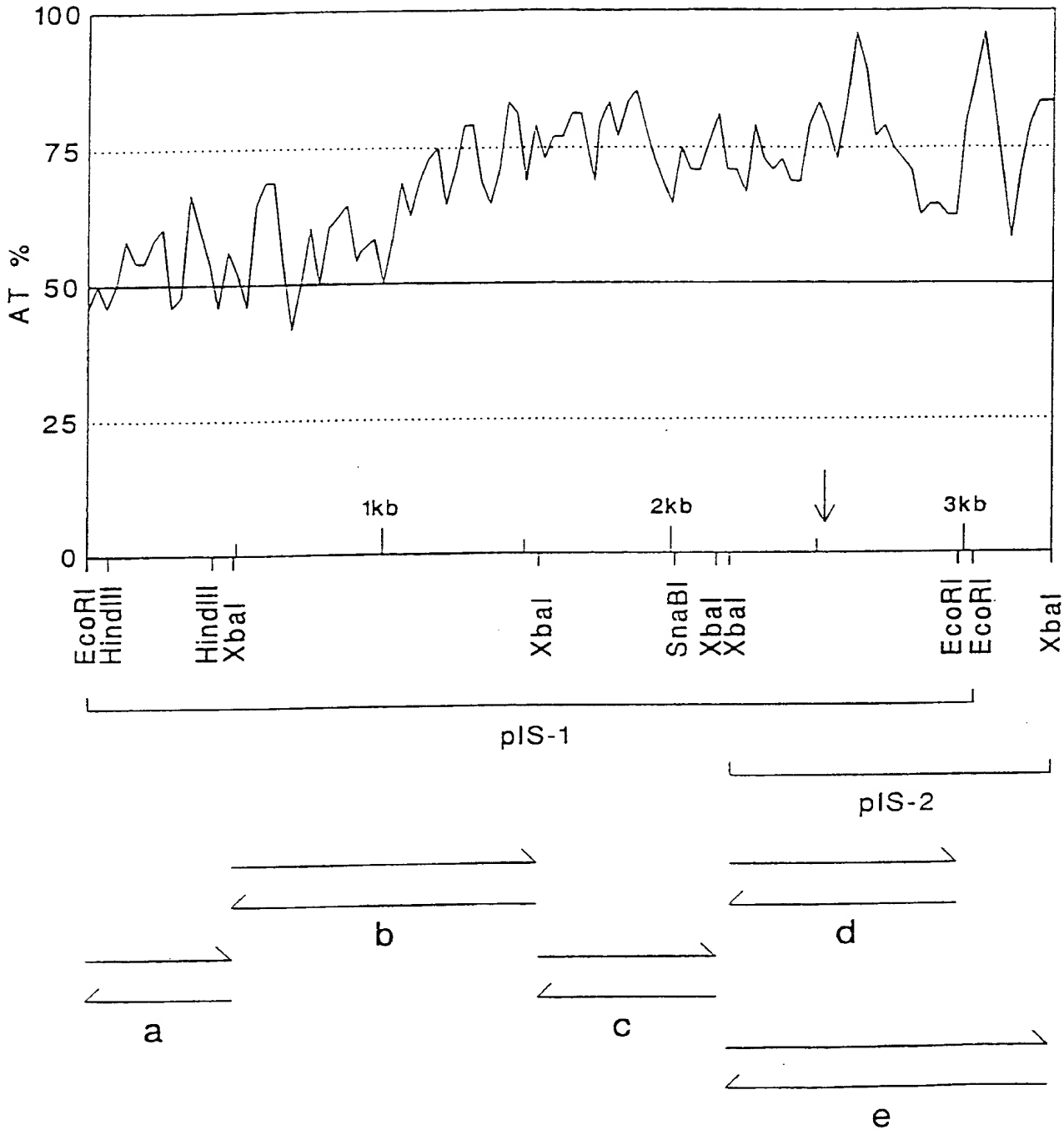

100
75
50
25
0
AT %
1kb
2kb
3kb
EcoRI
HindIII
HindIII
XbaI
XbaI
SnaBI
XbaI
XbaI
EcoRI
EcoRI
XbaI
pIS-1
pIS-2
a
b
c
d
e

FIGURE 7

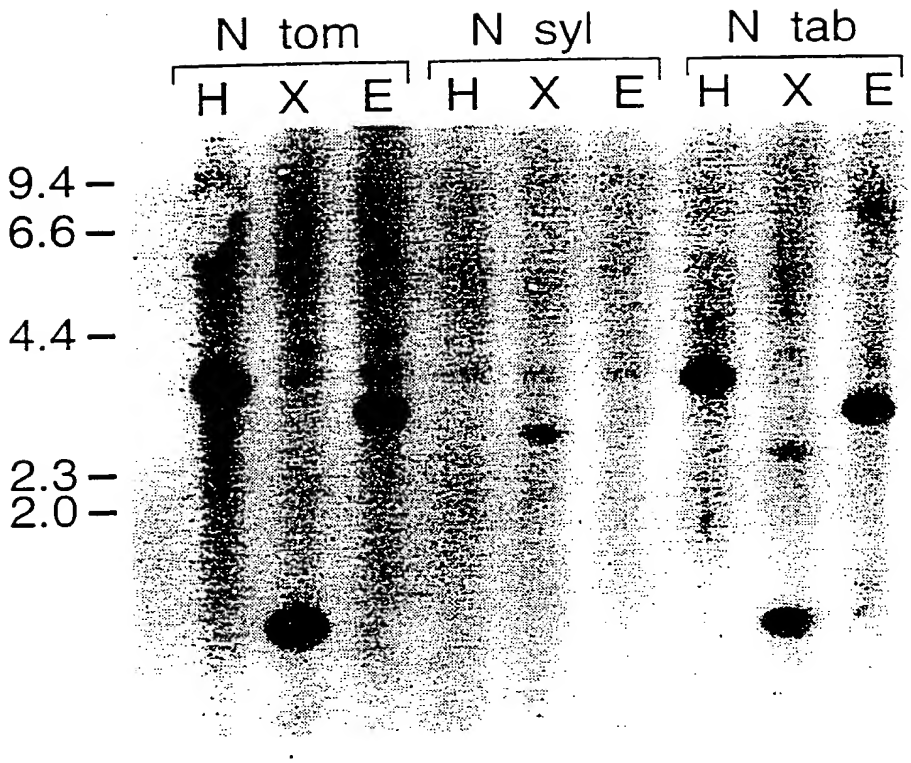


FIG. 8

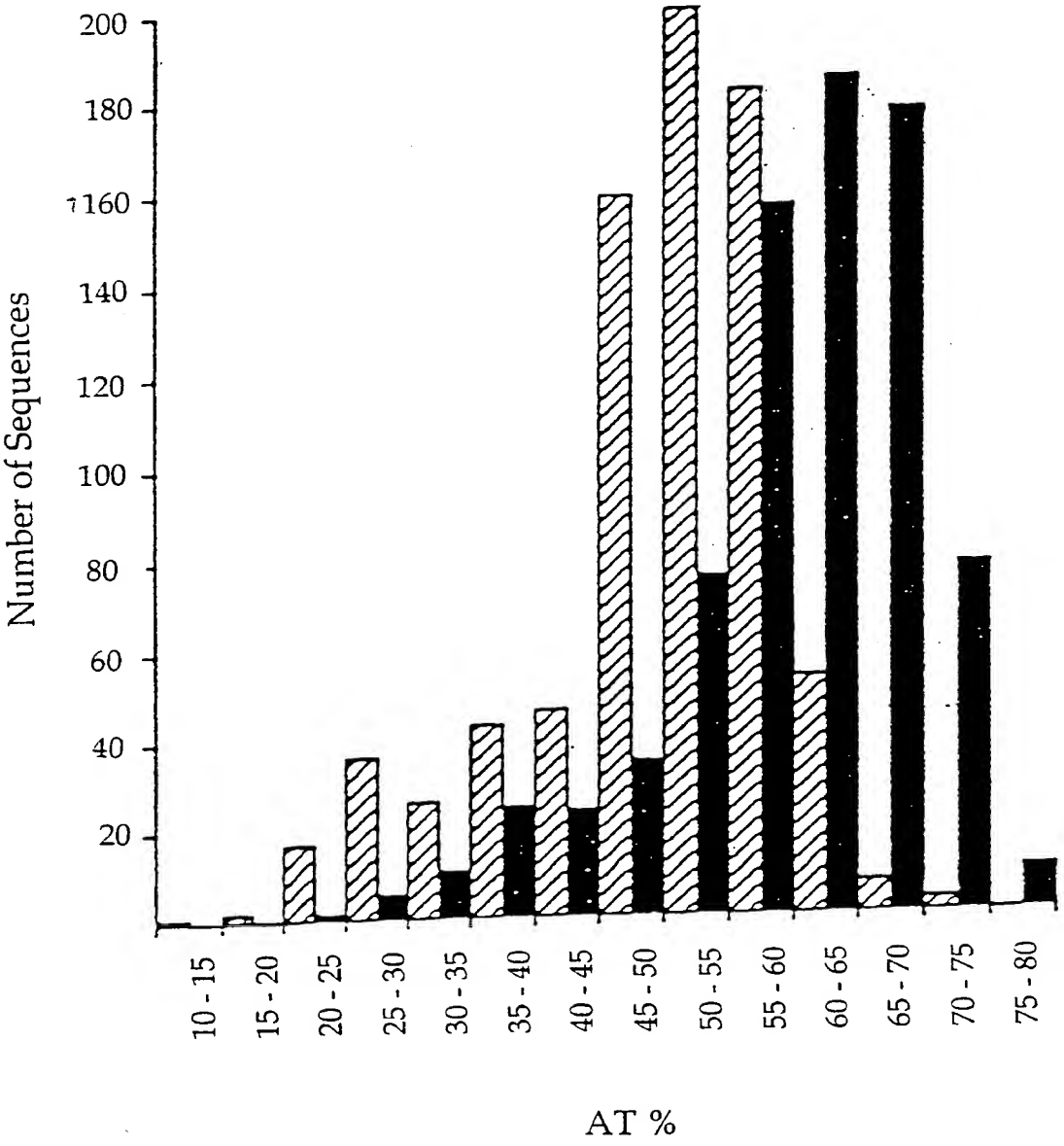

Number of Sequences
200
180
160
140
120
100
80
60
40
20
10 - 15
15 - 20
20 - 25
25 - 30
30 - 35
35 - 40
40 - 45
45 - 50
50 - 55
55 - 60
60 - 65
65 - 70
70 - 75
75 - 80
AT %

FIGURE 9

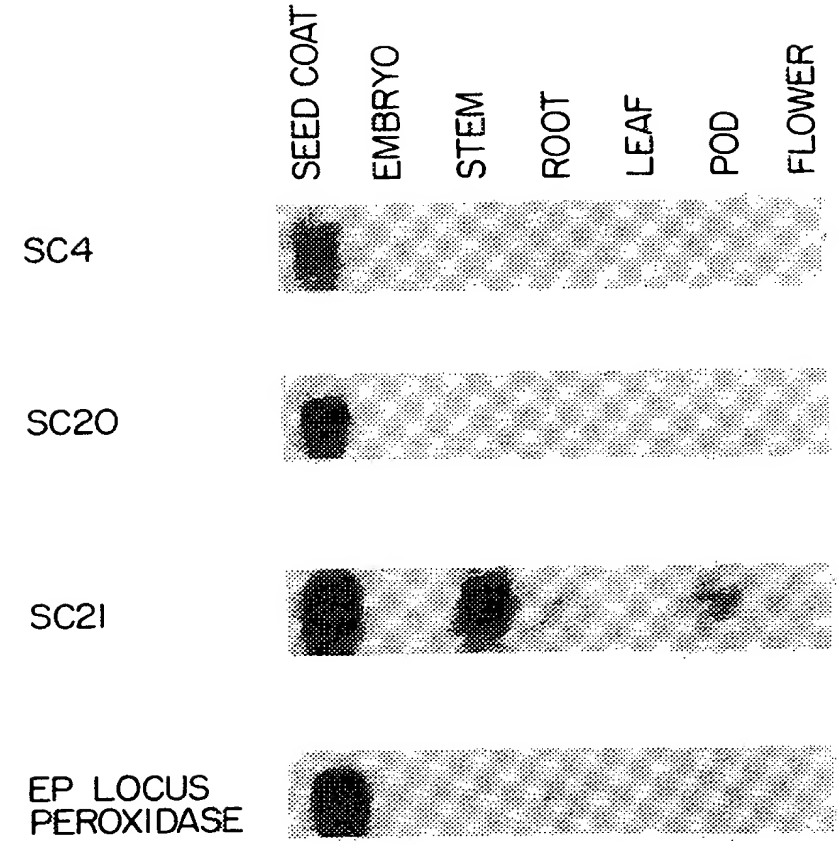


FIG. 10A

FIG. 10B

FIG. 10C

FIG. 10D

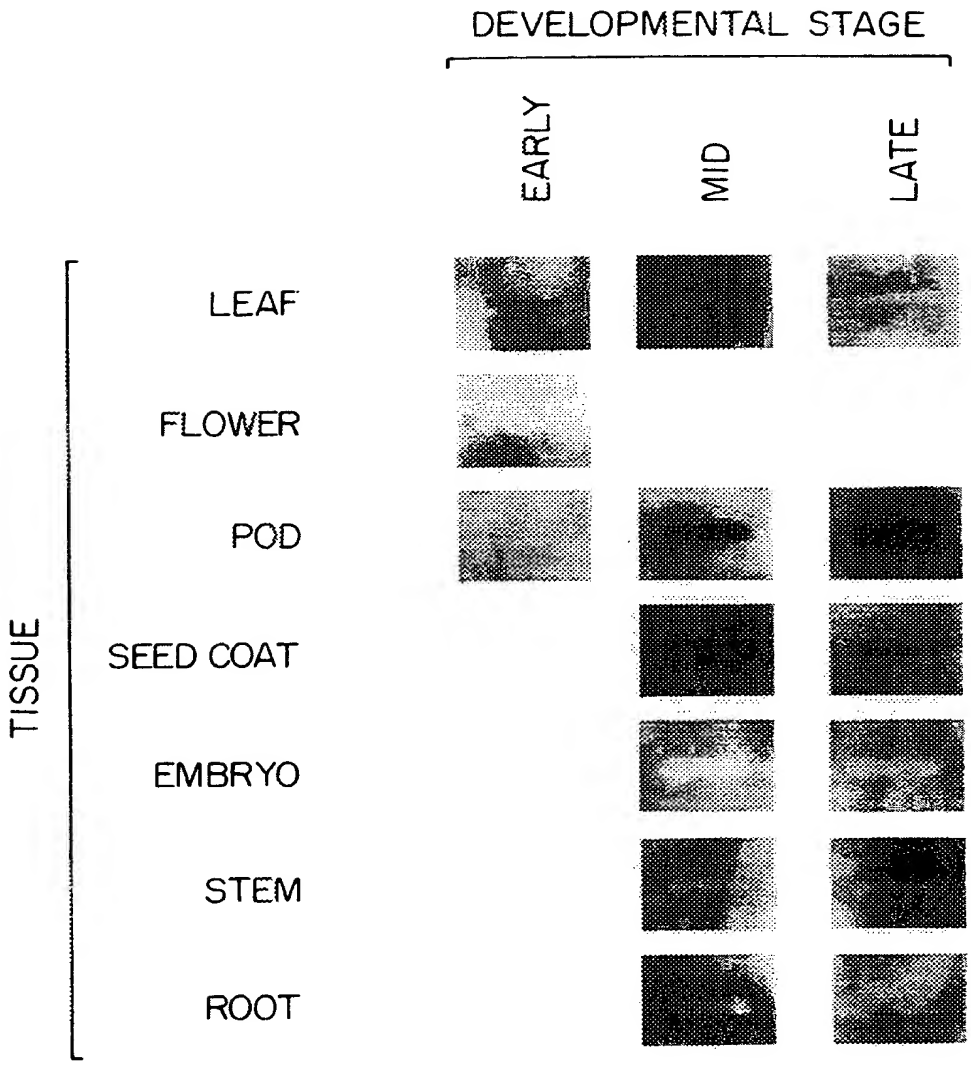

DEVELOPMENTAL STAGE
EARLY
MID
LATE
TISSUE
LEAF
FLOWER
POD
SEED COAT
EMBRYO
STEM
ROOT

FIG. 10E

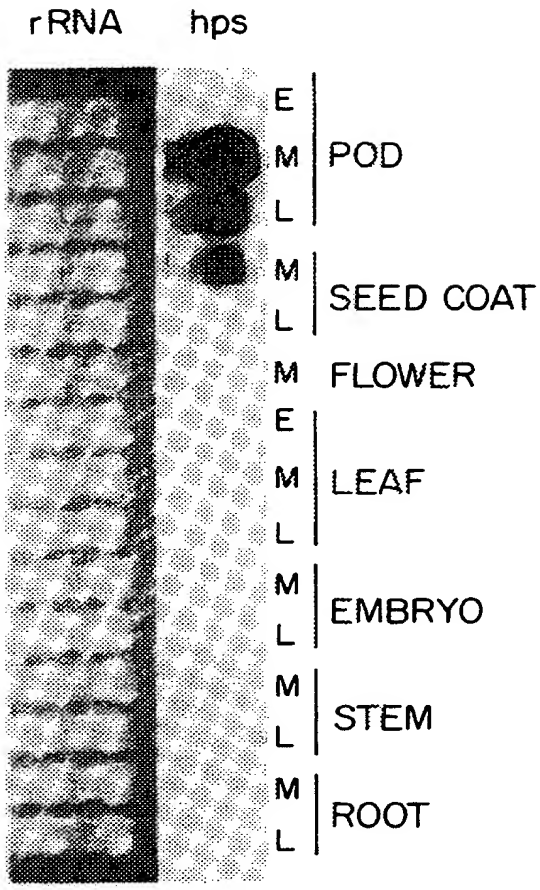


FIG. 10F

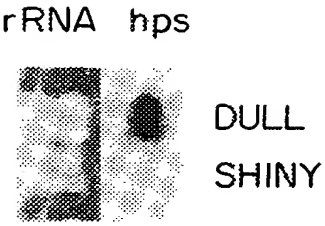


FIG. 10G

RESTRICTION MAP OF SC20

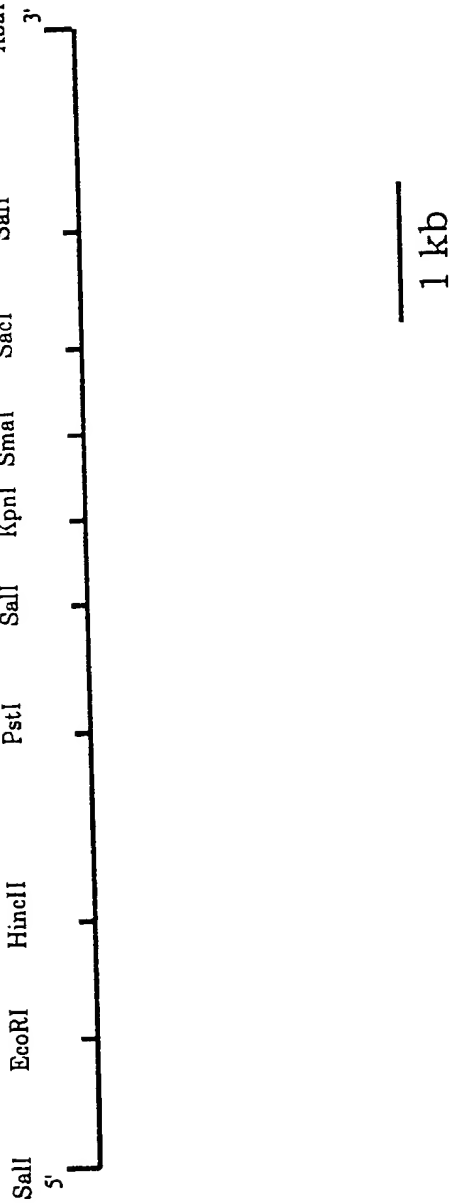


FIGURE 11(A)

RESTRICTION MAP OF SC21

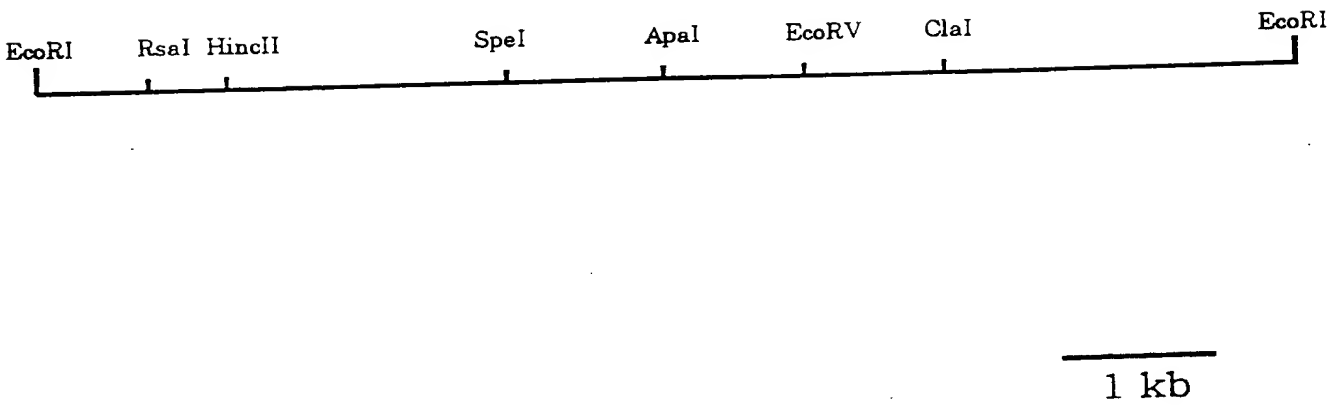


FIGURE 11(B)

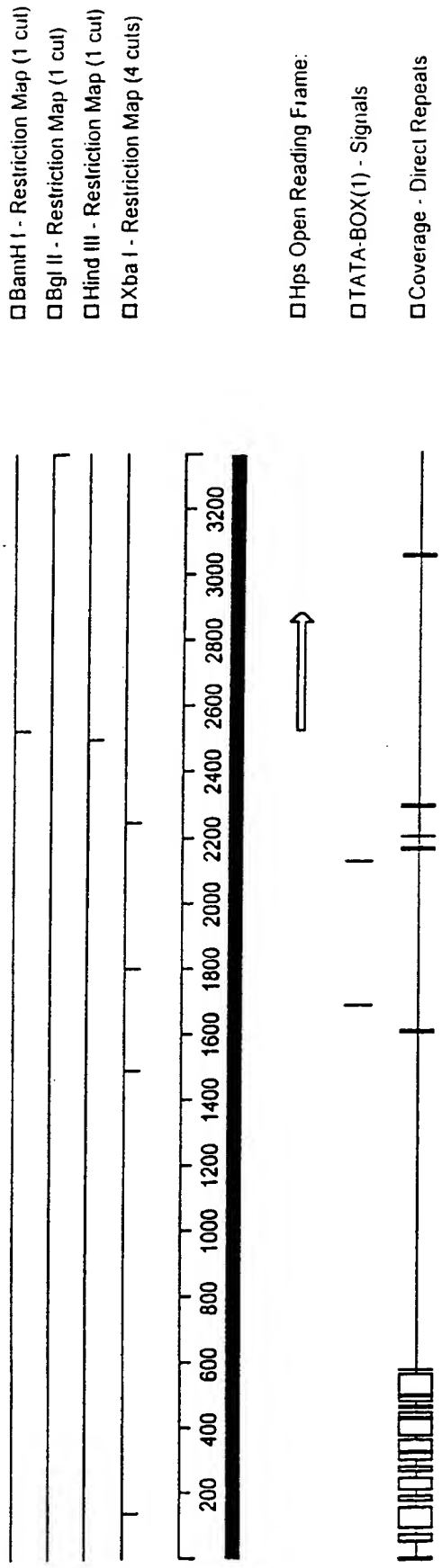
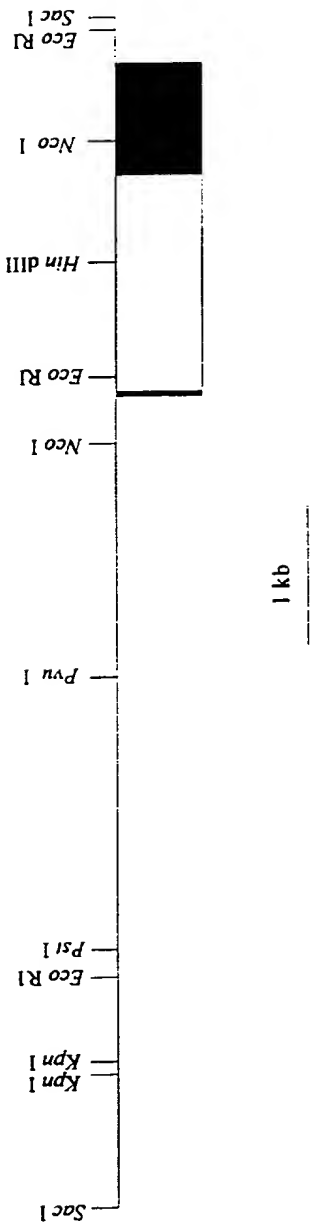

BamH I - Restriction Map (1 cut)
Bgl II - Restriction Map (1 cut)
Hind III - Restriction Map (1 cut)
Xba I - Restriction Map (4 cuts)
Hps Open Reading Frame:
TATA-BOX(1) - Signals
Coverage - Direct Repeats
200
400
600
800
1000
1200
1400
1600
1800
2000
2200
2400
2600
2800
3000
3200

FIGURE 11(C)



Restriction map of *sc4*

The shaded and open boxes represent exons and introns respectively.

FIG. 11(D)

6 DAF

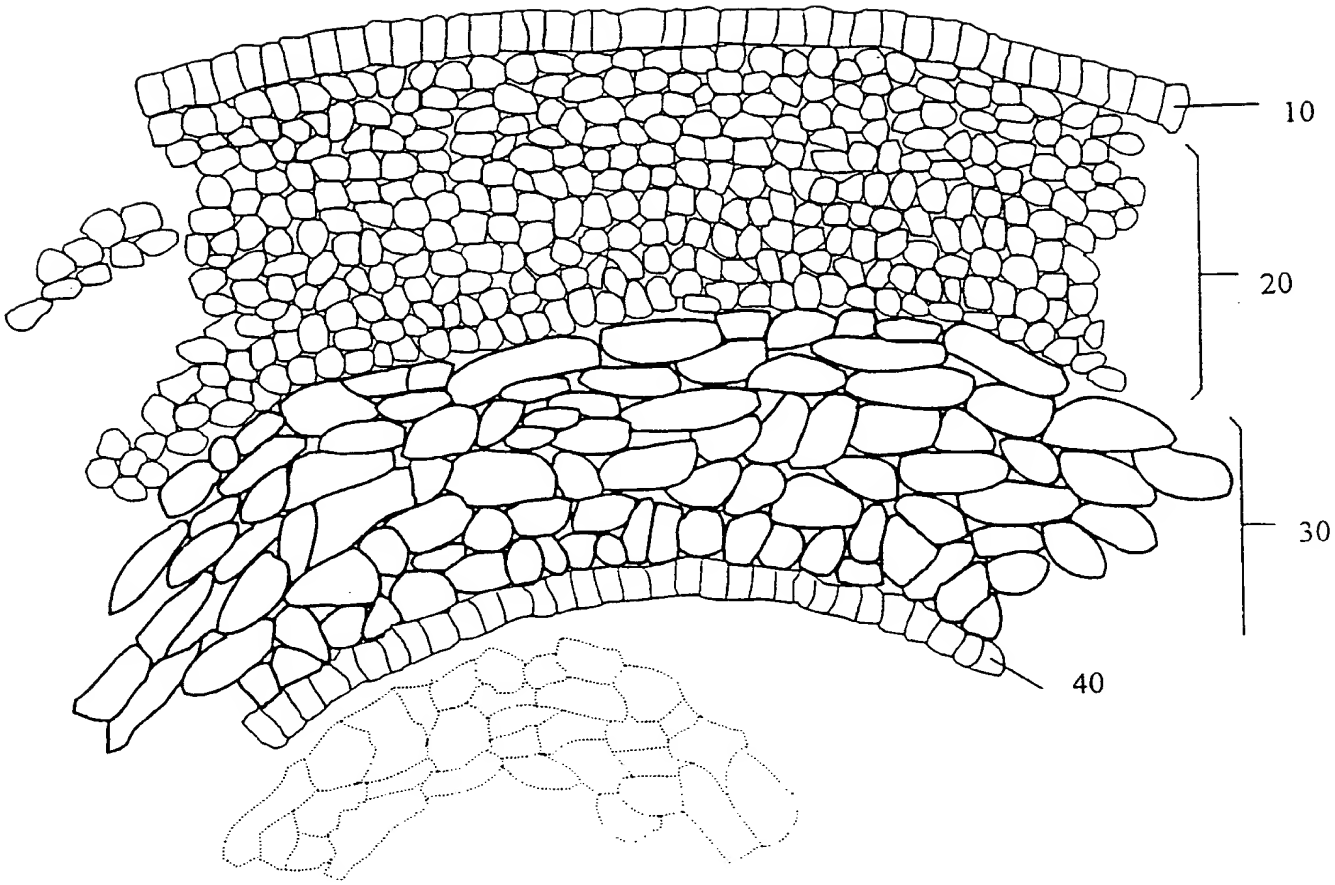


FIGURE 12(a)

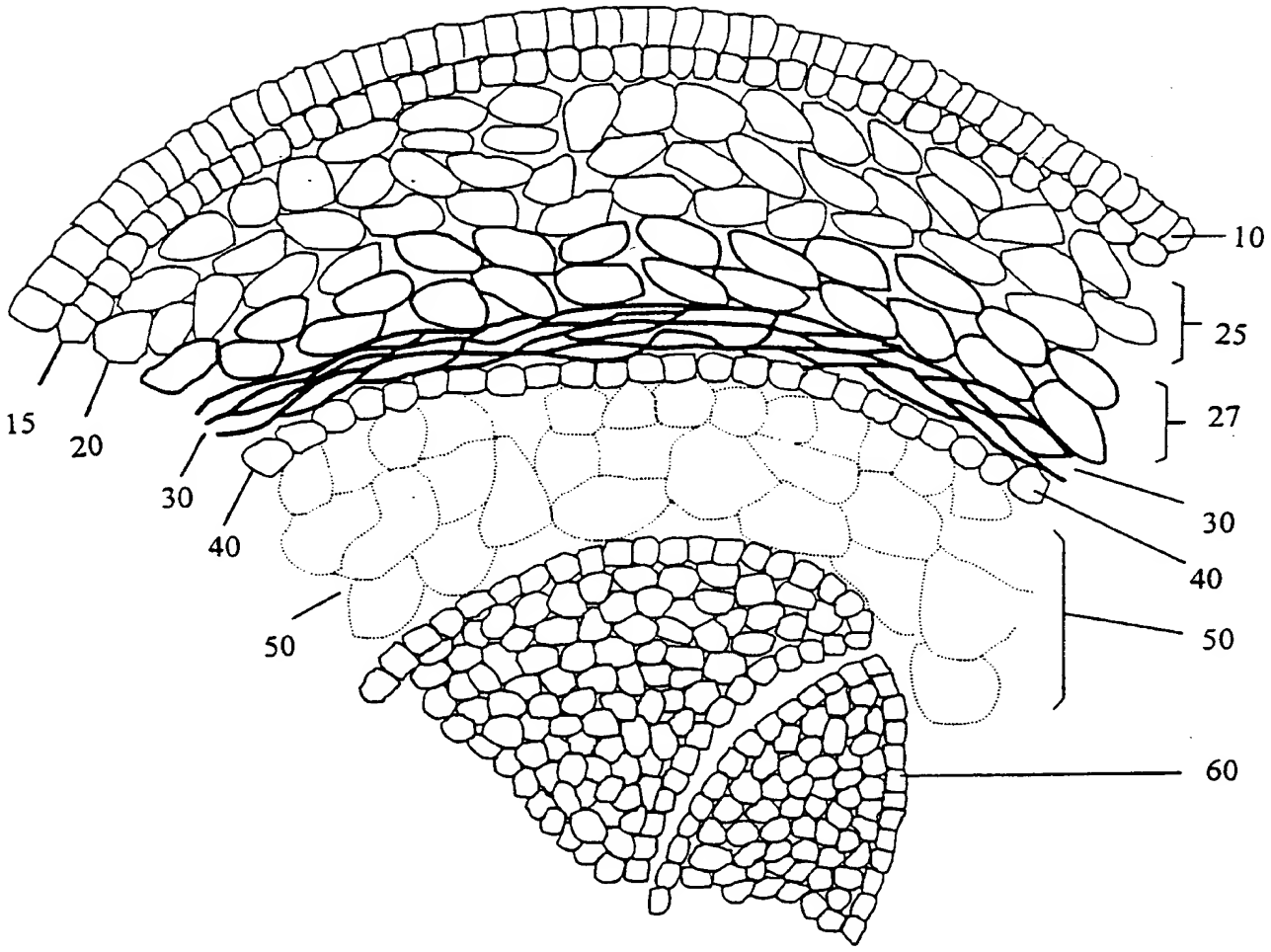


FIGURE 12(b)

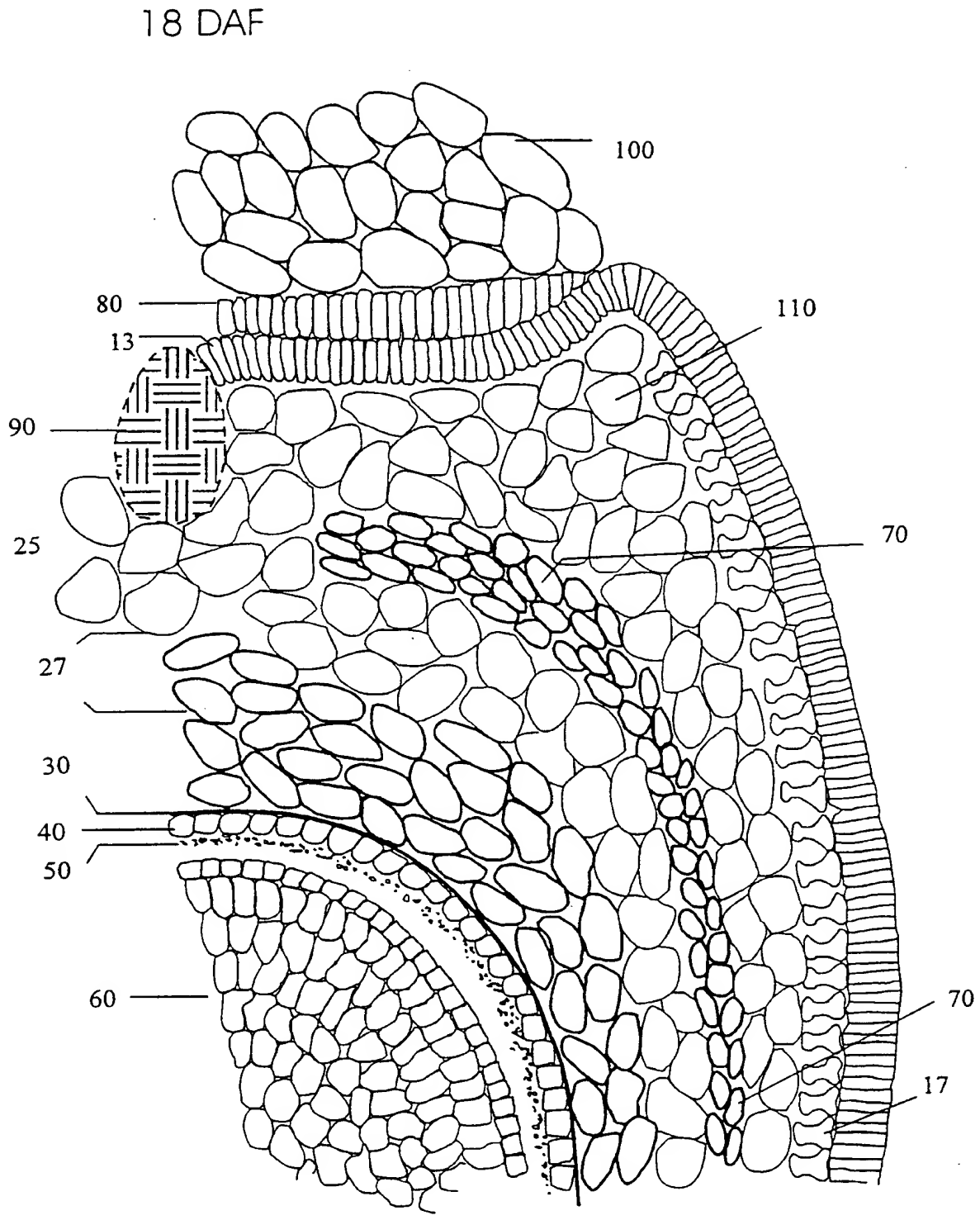


FIGURE 12(c)

FIG. 13A

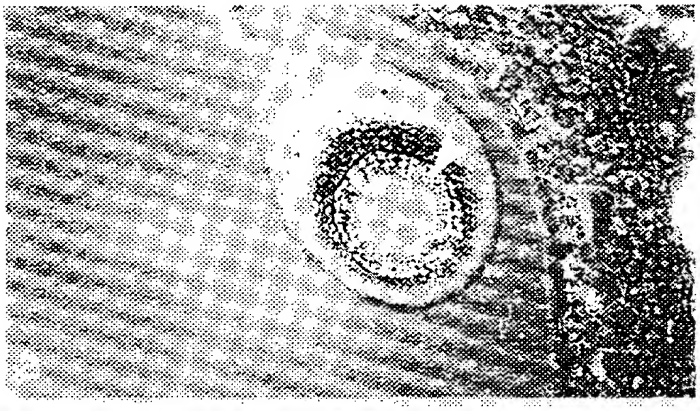


FIG. 13B

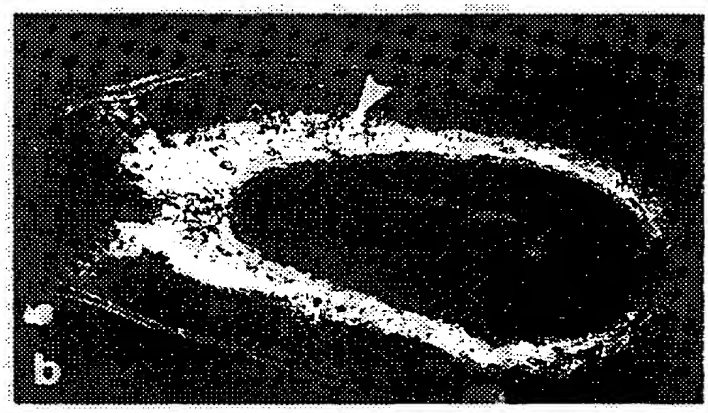


FIG. 13C

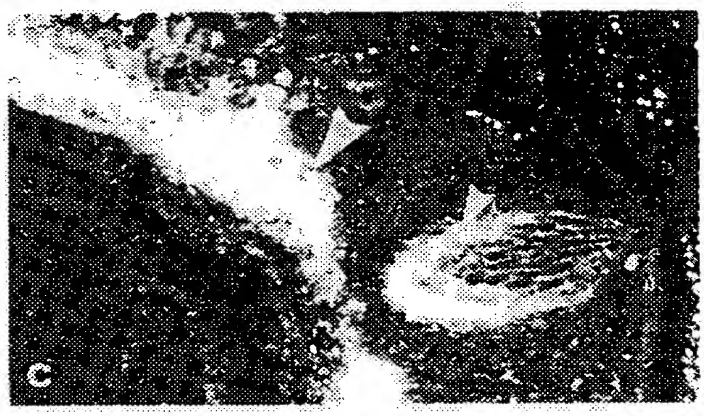


FIG. 13D

FIG. 13E

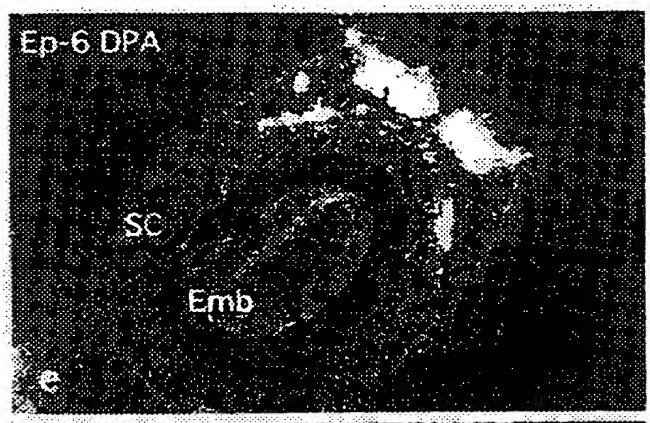
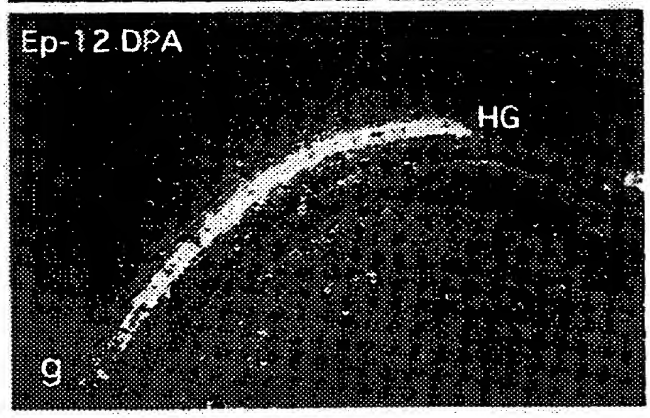


FIG. 13F

FIG. 13G



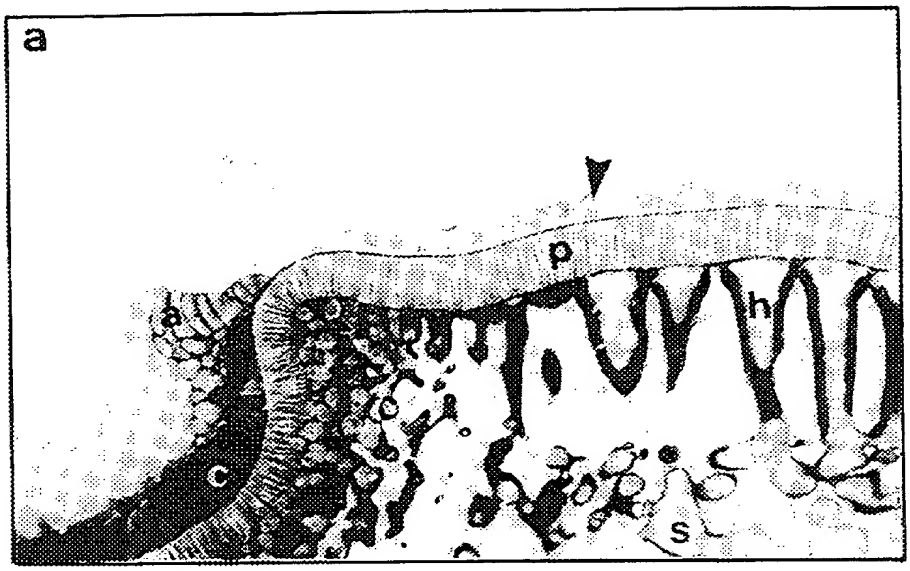


FIG. 14A

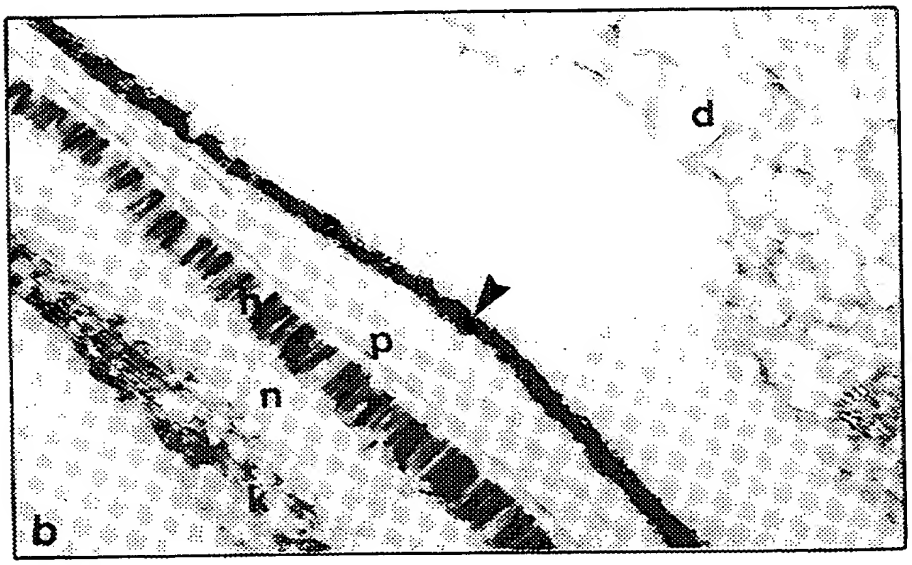


FIG. 14B

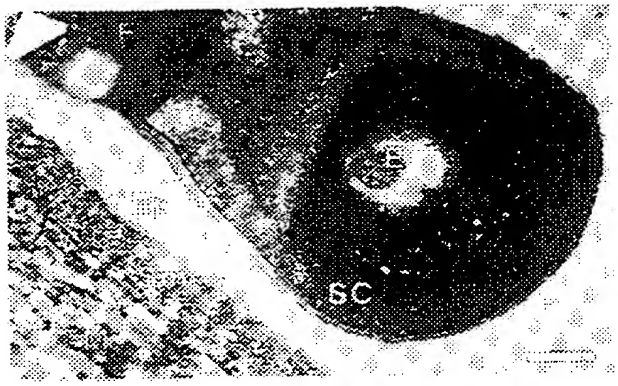


FIG. 14C

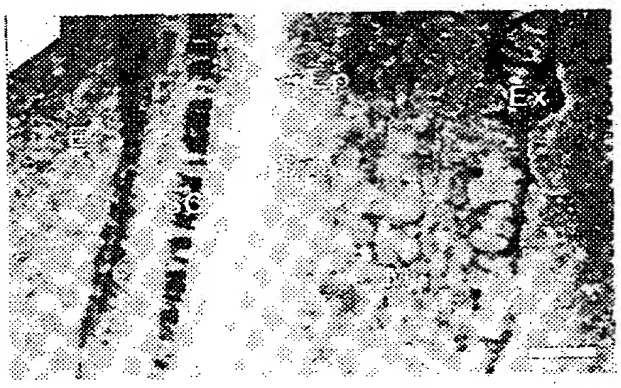


FIG. 14D

```
TAAGCTTTCAAGAGACAAACTGCTTTGAAAAATGGGATCCAAGGTTGTTGCATCCGTTGC      60
                                M  G  S  K  V  V  A  S  V  A      10

CCTTCTCCTCTCCATCAACATTCTTTTCATTTCCATGGTTAGCTCCAGCAGCCACTACGA     120
L  L  L  S  I  N  I  L  F  I  S  M  V  S  S  S  S  H  Y  D      30

TCCACAGCCCCAACCTTCTCACGTCACTGCTCTTATTACACGACCTAGTTGTCCGGATCT     180
P  Q  P  Q  P  S  H  V  T  A  L  I  T  R  P  S  C  P  D  L      50

GAGTATTTGCCTCAATATTTTAGGCGGGTCTCTAGGAACCGTGGATGATTGTTGTGCCCT     240
  S  I  C  L  N  I  L  G  G  S  L  G  T  V  D  D  C  C  A  L      70

CATCGGTGGTCTTGGTGACATTGAAGCCATTGTGTGCCTTTGCATCCAACTCAGGGCCCT     300
  I  G  G  L  G  D  I  E  A  I  V  C  L  C  I  Q  L  R  A  L      90

CGGAATATTAAACCTTAACCGTAATTTGCAGTTAATATTAAACTCCTGTGGACGAAGCTA     360
  G  I  L  N  L  N  R  N  L  Q  L  I  L  N  S  C  G  R  S  Y     110

CCCGTCAAACGCCACTTGCCCCCGAACCTAAGAACAGAATATGTATGGCACTAATTACCA     420
  P  S  N  A  T  C  P  R  T  *                                    119

TATTACTTCGTATCATGGTGTTTGTTTGTTTGTCTGTGTTTAAAGTTAAGGATGTTATAC     480

CCTTCGTGCCTGCTACATATATATAGTGGGCACTATAATATTACCAATAAATTAACGTCC     540

ATATATAAGAATAATAATAAATAAATAAATATTTCTATACAAATAAAGGTTACGTAATGT     600

TGTTGTTCTCGTGGATGGGGATCTTATCTTCCTCCTCGCTATCTTTGTTTATCGTATTTC     660

AGTGAAAGTTGTTCAATAAAAGTCCTTTGTTCAACAAGT(A)n                      700
```

FIGURE 15(A)

```
MGSKVVASVALLLSINILFISMVSS   25
SSHYDPQPQPSHVTALITRPSCPDL   50
SICLNILGGSLGTVDDCCALIGGLG   75
DIEAIVCLCIQLRALGILNLNRNLQ  100
LILNSCGRSYPSNATCPRT        119
```

FIG. 15(B)

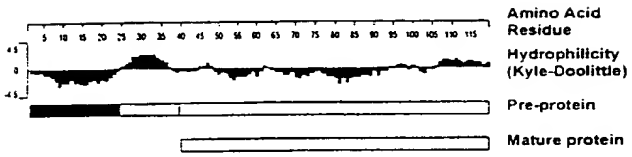


FIG. 15(C)

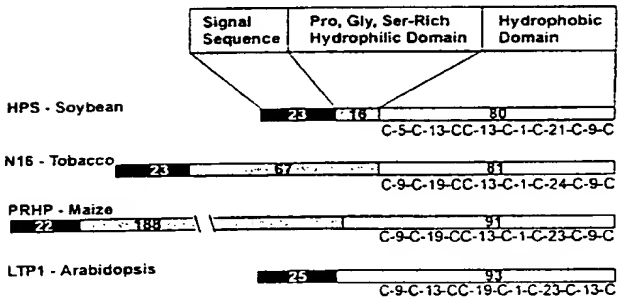


FIG. 15(D)

FIG. 15

CULTIVAR: CLARK
PHENOTYPE: DULL

WILLIAMS 82
SHINY

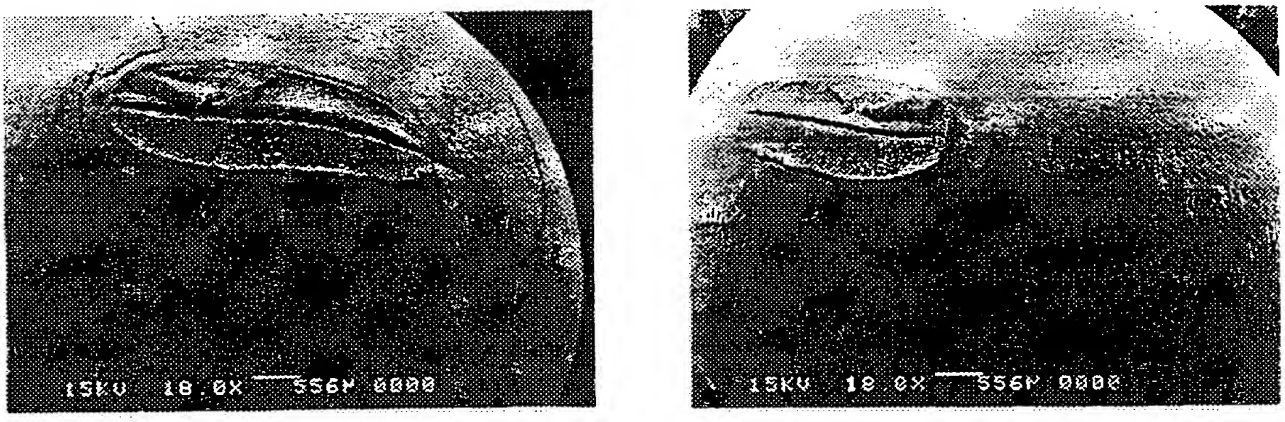


FIG. 16A

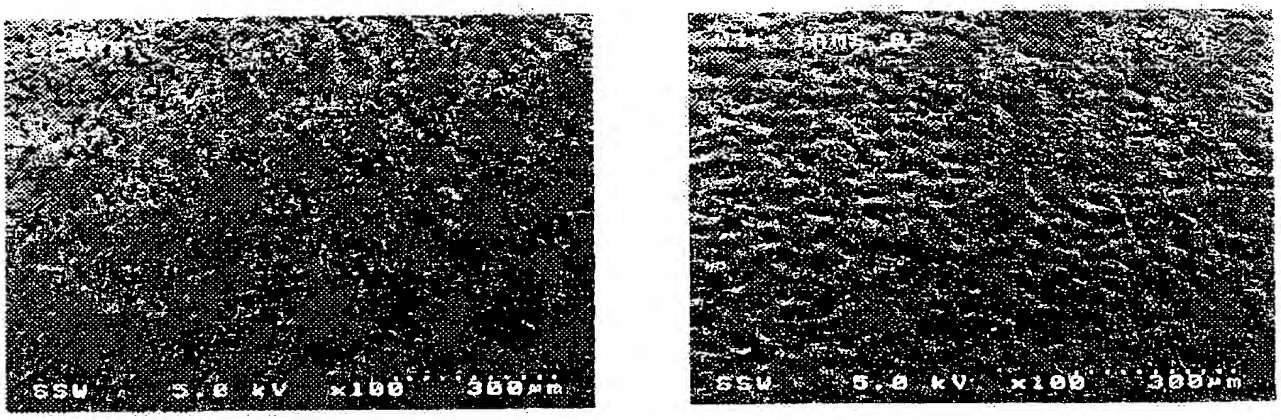


FIG. 16B

FIG. 16C

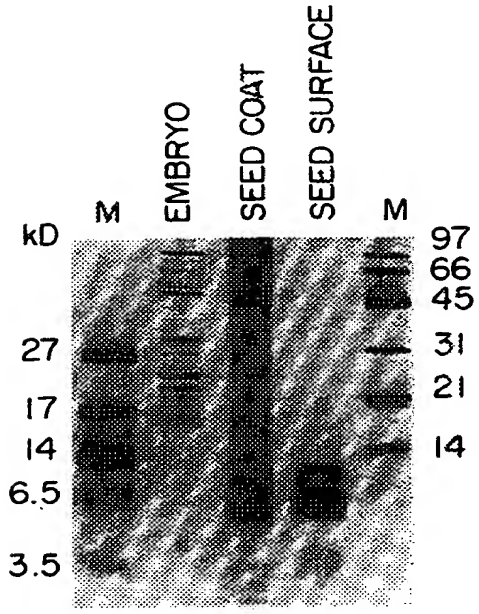


FIG. 17A

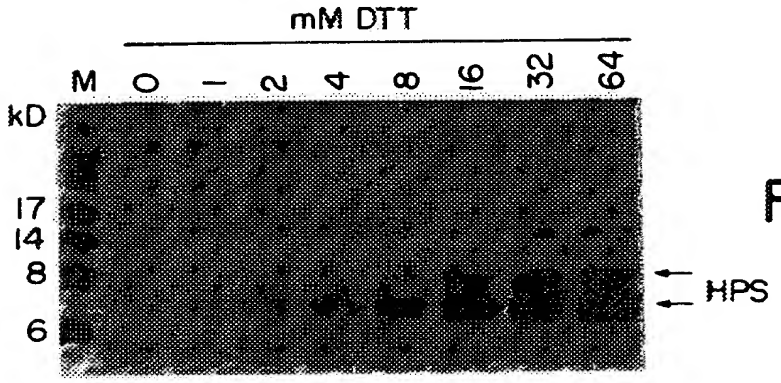


FIG. 17B

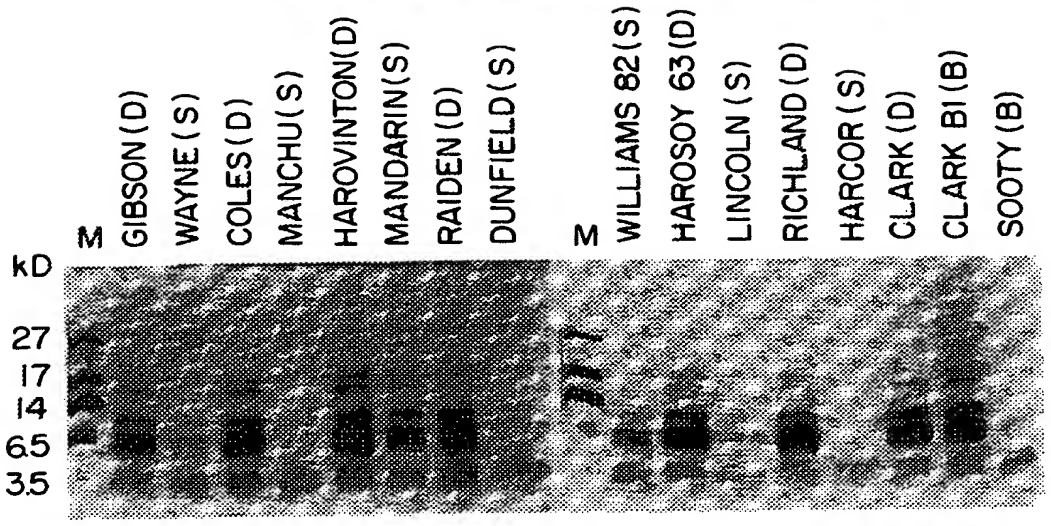


FIG. 17C

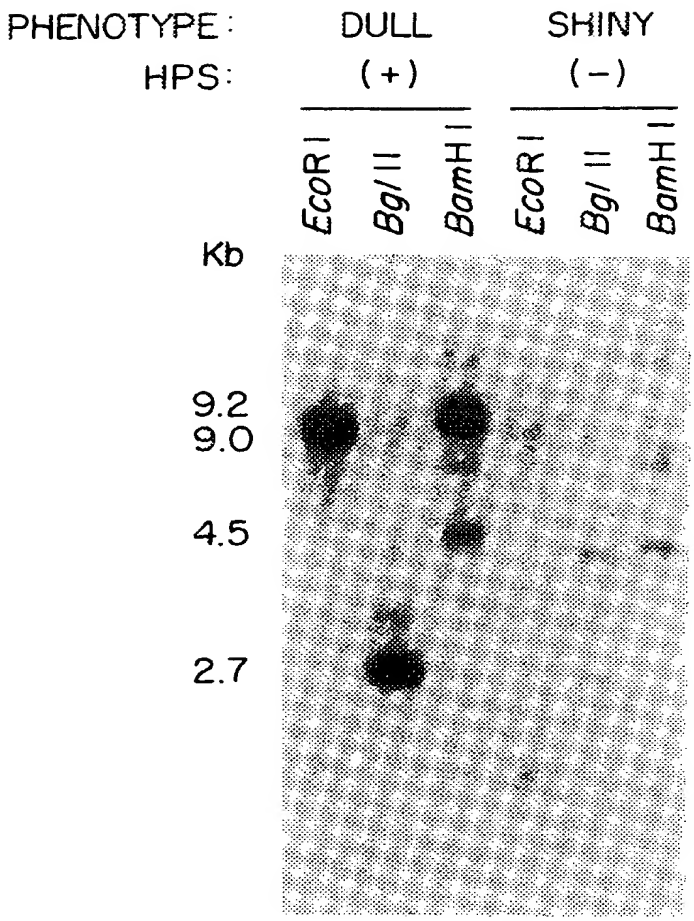


FIG. 18

```
--C AAT GCT GCG TTA ACT CCT AGA CAT TAC TGG GAA ACG ATG CTT CCA AGA ACT CCC   55
     N   A   A   L   T   P   R   H   Y   W   E   T   M   L   P   R   T   P   18

TTG CCG AAA GCA ATC ACA GAG CTA CTA AGC CTT GAA AGT AGG TCC ATA TTT GAA TAT  112
 L   P   K   A   I   T   E   L   L   S   L   E   S   R   S   I   F   E   Y   37

GCC GGG AAT GAT GAC CAG TCA GAA AGT AGG TCC ATA TTA GGA TAC GCT GGC TAT AAT  169
 A   G   N   D   D   Q   S   E   S   R   S   I   L   G   Y   A   G   Y   N   56

CAA GAC GAG GAT GAT GTG AGC AAA CAC AAT ATA CAA ATC TTC AAC AGG TTG TTT TTC  226
 Q   D   E   D   D   V   S   K   H   N   I   Q   I   F   N   R   L   F   F   75

TTG GAA GAG GAC CTG CGT GCT GGC AAA ATA TTC AAC ATG AAG TTC GTC AAC AAC ACA  283
 L   E   E   D   L   R   A   G   K   I   F   N   M   K   F   V   N   N   T   94

AAA GCC ACA GTC CCG TTG CTA CCG CGC CAA ATT TCG AAA CAA ATA CCG TTC TCA GAA  340
 K   A   T   V   P   L   L   P   R   Q   I   S   K   Q   I   P   F   S   E   113

GAT AAA AAG AAG CAA GTG TTG GCG ATG CTT GGC GTG GAA GCG AAC TCA AGC AAC GCC  397
 D   K   K   K   Q   V   L   A   M   L   G   V   E   A   N   S   S   N   A   132

AAG ATC ATA GCG GAG ACC ATT GGT CTT TGC CAA GAG CCT GCA ACG GAG GGA GAA AGG  454
 K   I   I   A   E   T   I   G   L   C   Q   E   P   A   T   E   G   E   R   151

AAA CAC TGC GCG ACT TCG TTG GAG TCC ATG GTT GAT TTC GTC GTT TCC GCG CTC GGG  511
 K   H   C   A   T   S   L   E   S   M   V   D   F   V   V   S   A   L   G   170

AAG AAC GTT GGT GCT TTC TCA ACA GAG AAA GAA AGG GAA ACT GAG TCT GGA AAG TTT  568
 K   N   V   G   A   F   S   T   E   K   E   R   E   T   E   S   G   K   F   189

GTA GTG GTG AAA AAT GGG GTG AGG AAG TTG GGA GAT GAT AAG GTT ATT GCC TGT CAT  625
 V   V   V   K   N   G   V   R   K   L   G   D   D   K   V   I   A   C   H   208

CCA ATG AGT TAC CCT TAT GTT GTG TTT GGG TGT CAT CTA GTG CCA AGG AGT AGC GGG  682
 P   M   S   Y   P   Y   V   V   F   G   C   H   L   V   P   R   S   S   G   227

TAT TTG GTG CGC TTG AAG GGA GAA GAT GGG GTT CGA GTG AAA GCA GTT GTT GCG TGC  739
 Y   L   V   R   L   K   G   E   D   G   V   R   V   K   A   V   V   A   C   246

CAC AGA GAC ACG TCA AAG TGG GAC CAT AAT CAT GGG GCA TTC AAA GTG CTC AAT CTT  796
 H   R   D   T   S   K   W   D   H   N   H   G   A   F   K   V   L   N   L   265

AAG CCT GGG AAT GGT ACA GTA TGC CAT GTC TTC ACT GAG GGG AAT CTT CTT TGG CTT  853
 K   P   G   N   G   T   V   C   H   V   F   T   E   G   N   L   L   W   L   284

CCA AAT TAG attaattaccatatacatatttgtccttgttctatccttaaataagtggaatcacctgaagaa  925
 P   N   *                                                                   286

ttgtgcgtaatgagttgtttgtctttgtggaaattgttatctgtcttgcatcaccaaataggtatatataaaata 1000

acaggagcgtggtatttgttgcacaaaaatggatttcaaccgatcaaaaaaatatagcctttaccaattagaagg 1075

gtttggctttgttagcaaataataaaaataaaatatcttgatgg(a)n                           1119
```

FIG. 19(A)

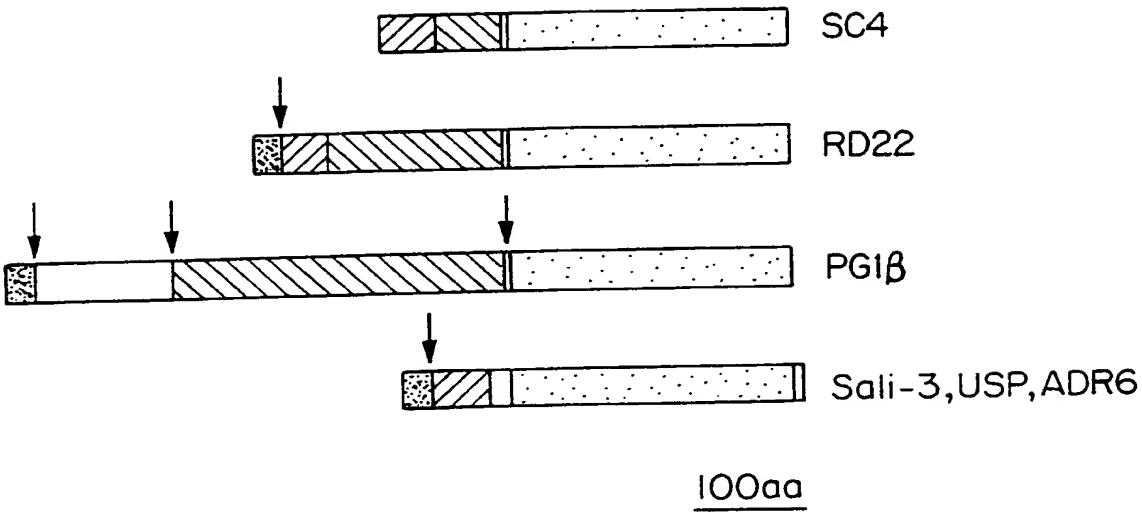
A

```
SC4c        FFLEEDLRAG KIFNMKFVNN --TKATVPLL PRQISKQIPF SEDKKKQVLA MLGVEANSSN 131
RD22        FFLEKDLVRG KEMNVRFNAE DGYGGKTAFL PRGEAETVPF GSEKFSETLK RFSVEAGSEE 235
PG1B        FFREKMLKSG TIMPMPDIK- -DKMPKRSFL PRVIASKLPF STSKIAELKK IFHAGDESQV 472
Sali3-2     FFYKEDLHPG KTMKVQFTKR ---------- --------PY AQPY--GVYT WLTDIKDTSK 215
USP         FF-EHDLHPG KNFNLGHTNS VGSIIR---- --------PF TKSR--QGVT --DSIWLANK 111
ADR6        FFYKEDLHPG KTMKVQFSKP ---------- --------PF QQPW--GVGT WLKEIKDTTK 111

SC4c        AKIIAETIGL CQE-PATEGE RKHCATSLES MVDFVVSALG KN-VGAFSTE KERETESGK- 188
RD22        AEMMKKTIEE C-EARKVSGE EKYCATSLES MVDFSVSKLG KYHVRAVSTE VAKKNAPMQK 294
PG1B        EKMIGDALSE C-ERAPSAGE TKRCVNSAED MIDFATSVLG RN-VVVRTTE DTKGSNGNIM 530
Sali3-2     EGYSFEEI-- CIKKEAFEGE EKFCAKSLGT VIGFAISKLG KN-IQVLSSS FVNKQE---- 168
USP         EKQSLEDF-- CYSPTAI-AE HKHCVSSLKS MIDQVISHFG STKIKAISSN FAPYQD---- 164
ADR6        EGYSFEEL-- CIKKEAIEGE EKFCAKSLGT VIGFAISKLG KN-IQVLSSS FVNKQD---- 164

SC4c        FVVVKNGVRK LGDDKVIACH PMSYPYVVFG CHLVPR-SSG YLVRLKGEDG VR-VKAVVAC 246
RD22        YKIAAAGVKK LSDDKSVVCH KQKYPFAVFY CHKAMM-TTV YAVPLEGENG MR-AKAVAVC 352
PG1B        I-GSVKGING GKVTKSVSCH QTLYPYLLYY CHSVPKVRVY EADILDPNSK VKINHGVAIC 589
Sali3-2     -QYTVEGVQN LG-DKAVMCH GLNFRTAVFY CHKV-RETTA FVVPLVAGDG TK-TQALAVC 224
USP         -QYVVEDVKK VG-DNAVMCH RLNFEKVVFN CHQV-RDTTA YVVSLVASDG TK-TKALTVC 220
ADR6        -QYTVEGVQN LG-DKAVMCH RLNFRTAVFY CHEV-RETTA FMVPLVAGDG TK-TQALAIC 220

SC4c        HRDTSKWDHN HGAFKVLNLK PGNGTVCHVF TEGNLLWLPN *                   286
RD22        HKNTSAWNPN HLAFKVLKVK PGTVPVCHFL PETHVVWFSY *                   392
PG1B        HVDTSSWGPS HGAFVALGSG PGKIEVCHWI FENDMTWAIA D*                          630
Sali3-2     HSDTSGMNH- HILHELMGVD PGTNPVCHFL GSKAILWVPN ISMDTAYQTN VVV*  276
USP         HHDTRGMNP- ELLYEALEVT PGTVPVCHFI GNKAAAWVPN HTADNLCVM*                  268
ADR6        HSNTSGMNH- QMLHQLMGVD PGTNPVCHFL GSKAILWVPN LSVDTAYQTN IVA*  272
```

B

```
SC4c        --NAALTPRL YWETMLPRTP LPKAITELLS L  29
RD22        AIAADLTPER YWSTALPNTP IPNSLHNLLT F  48
Sali3-2     HVHASLPEED YWEAVWPNTP IPTALRDVLK P  53
USP         GITATSSGED YWQSIWPNTP LPKTFSDLLI P  48
ADR6        ARESHARDED FWHAVWPNTP IPSSLRDLLK P  49
```

FIG. 19(B)



HYDROPHOBIC REGION:
CONSERVED SEGMENT:
REPEATED REGION:
BURP DOMAIN:
PEPTIDE CLEAVAGE POINT:

FIG. 19C

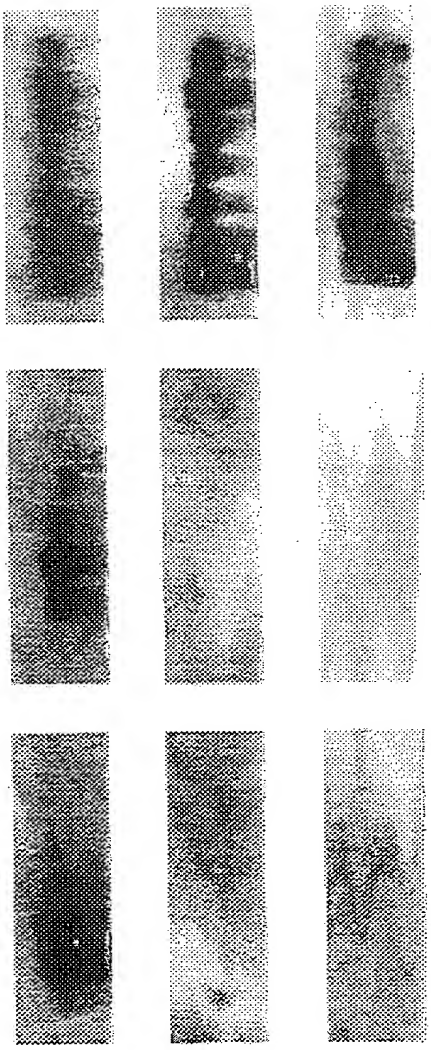


Fig. 20 A

Fig. 20 B

Fig. 20 C

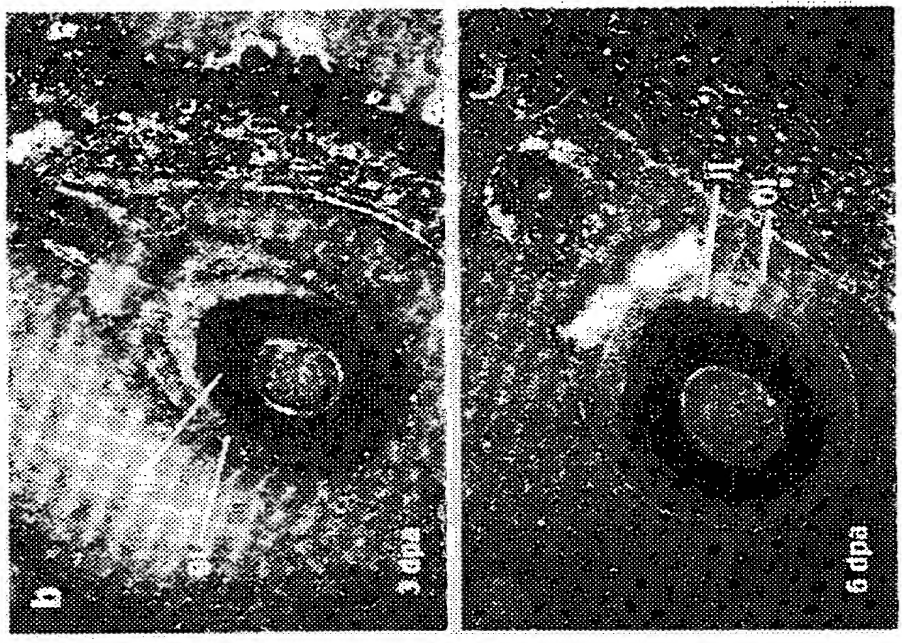


FIG. 2IB

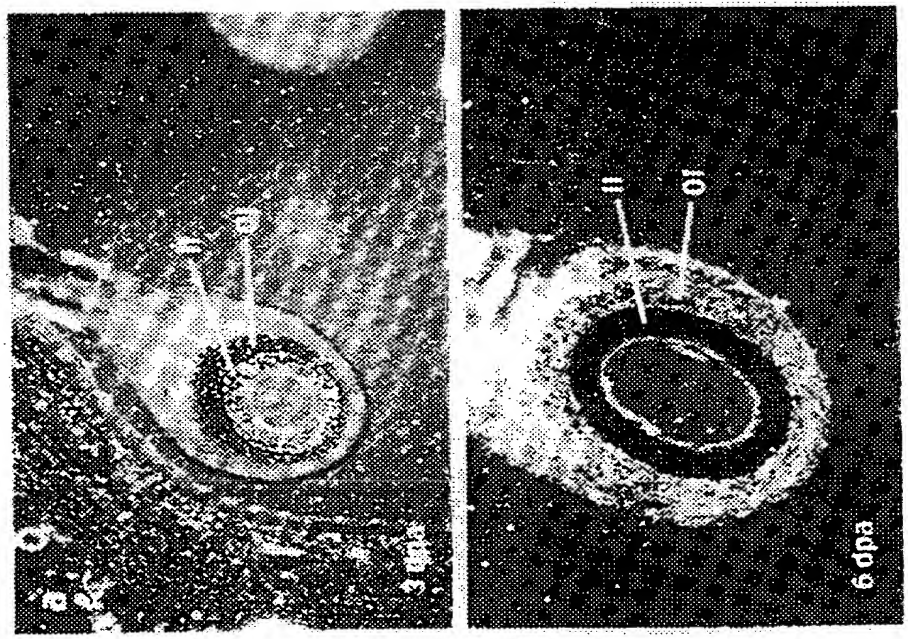
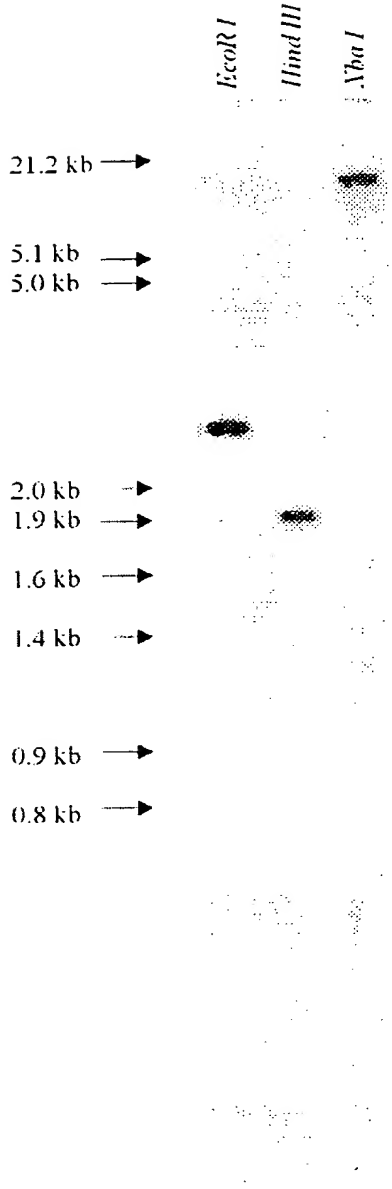


FIG. 2IA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Xba I
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5.0 kb
2.0 kb
1.9 kb
1.6 kb
1.4 kb
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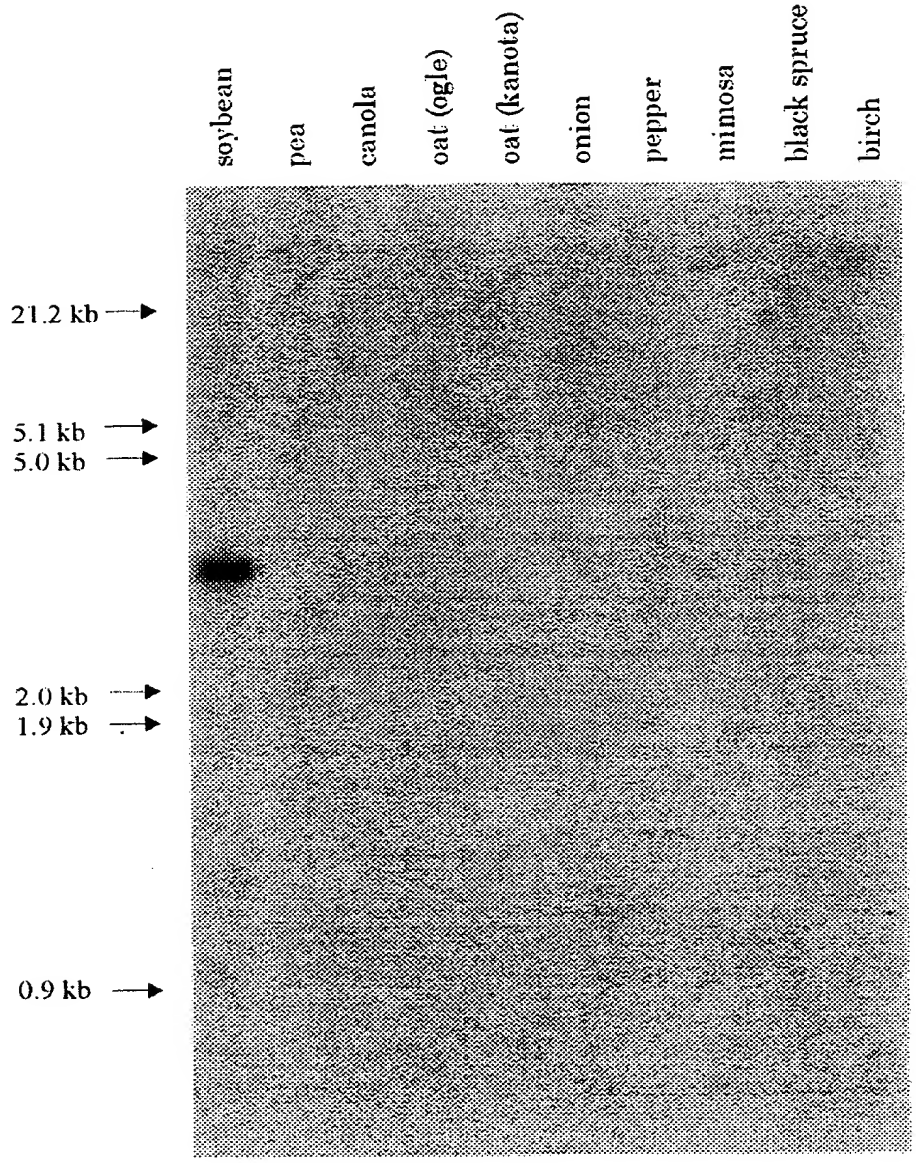
0.8 kb

Fig. 22 A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pea
canola
oat (ogle)
oat (kanota)
onion
pepper
mimosa
black spruce
birch
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5.1 kb
5.0 kb
2.0 kb
1.9 kb
0.9 kb

Fig. 22 B

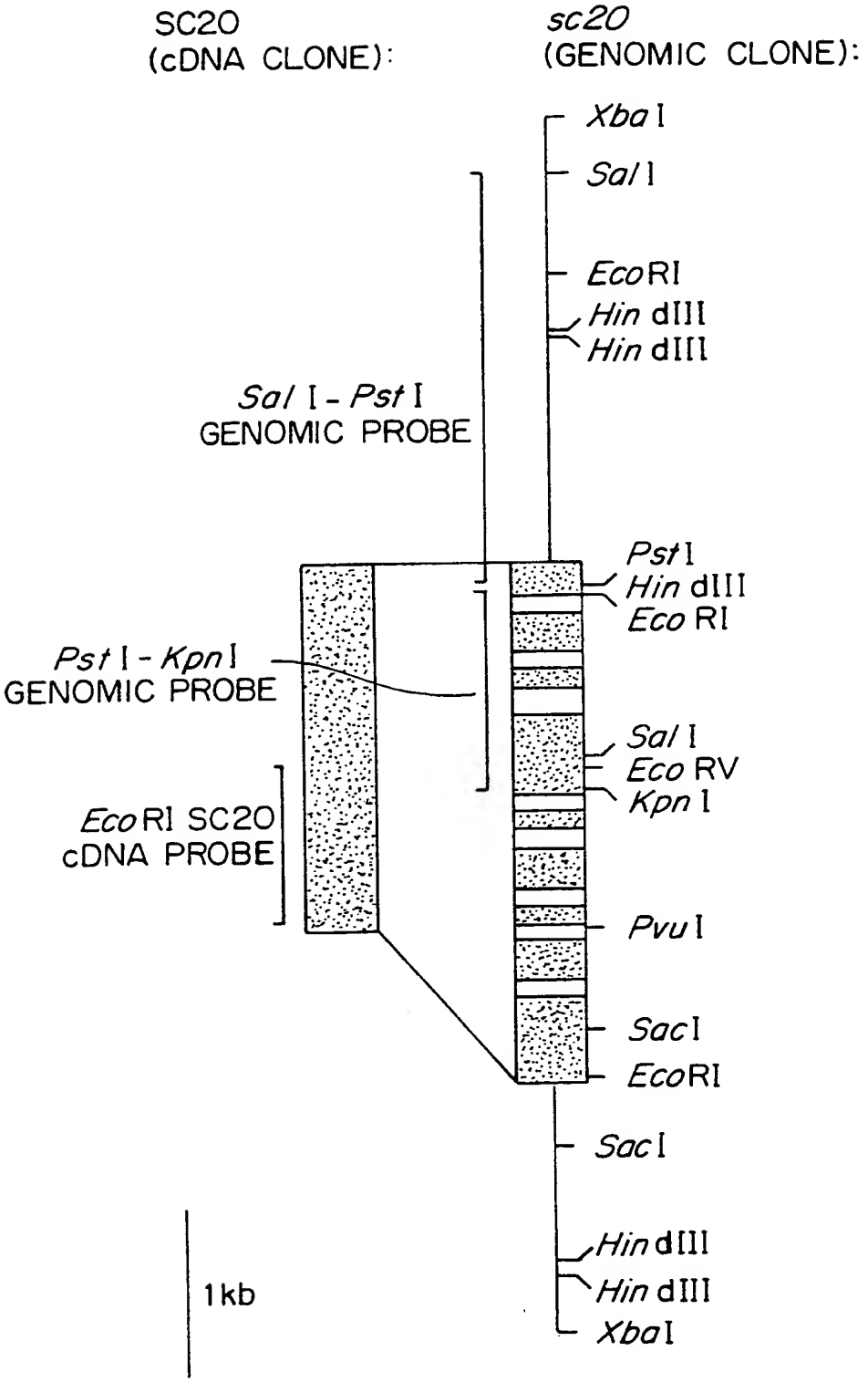

SC20
(cDNA CLONE):
sc20
(GENOMIC CLONE):
Xba I
Sal I
EcoRI
Hin dIII
Hin dIII
Sal I - Pst I
GENOMIC PROBE
Pst I
Hin dIII
Eco RI
Pst I - Kpn I
GENOMIC PROBE
Sal I
Eco RV
Kpn I
EcoRI SC20
cDNA PROBE
Pvu I
Sac I
EcoRI
Sac I
Hin dIII
Hin dIII
Xba I
1kb

FIG. 23A

```
caaagttttaac ATG AAA GGC AAT AAT ACA CTT TTG TTG CAT TTA TTC TAC ACT ACT CTC  60
             M   K   G   N   N   T   L   L   L   H   L   F   Y   T   T   L   16

TTC CTG TTT CTT GTA GTG TCA AGT TCA TCT TCA ACA GGG AAT GAA AGT AAC GAT GAC  117
F   L   F   L   V   V   S   S   S   S   S   T   G   N   E   S   N   D   D   35

ACT AAC AGT AAA GAA GTT TAT ATC GTG TAC ATG GGA GCT GCA GAT TCA ACA AAA GCT  174
T   N   S   K   E   V   Y   I   V   Y   M   G   A   A   D   S   T   K   A   54

TCT CTT AAA AAT GAG CAC GCT CAG ATT CTG AAT TCA GTG CTA AGA AGG AAT GAG AAT  231
S   L   K   N   E   H   A   Q   I   L   N   S   V   L   R   R   N   E   N   73

GCC CTA GTA CGG AAC TAC AAG CAT GGT TTC TCT GGG TTC GCA GCT CGT CTA TCA AAA  288
A   L   V   R   N   Y   K   H   G   F   S   G   F   A   A   R   L   S   K   92

GAG GAG GCA AAC TCA ATT GCT CAG AAA CCT GGT GTG GTG TCT GTT TTC CCT GAC CCC  345
E   E   A   N   S   I   A   Q   K   P   G   V   V   S   V   F   P   D   P   111

ATT CTG AAG CTC CAC ACT ACA CGT TCA TGG GAT TTC CTC AAA AGC CAA ACT CGT GTC  402
I   L   K   L   H   T   T   R   S   W   D   F   L   K   S   Q   T   R   V   130

AAT ATC GAC ACC AAA CCA AAT ACG CTG TCC GGT TCT TCT TTT TCT TCA TCA GAC GTC  459
N   I   D   T   K   P   N   T   L   S   G   S   S   F   S   S   S   D   V   149

ATT CTT GGC GTC TTA GAC ACA GGC ATA TGG CCA GAG GCG GCG AGT TTT AGC GAC AAG  516
I   L   G   V   L   D   T   G   I   W   P   E   A   A   S   F   S   D   K   168

GGT TTC GGT CCT GTT CCA TCC CGA TGG AAA GGC ACC TGC ATG ACA TCA AAA GAC TTC  573
G   F   G   P   V   P   S   R   W   K   G   T   C   M   T   S   K   D   F   187

AAT TCC TCT TGT TGT AAC AGG AAG ATA ATT GGC GCG AGG TTT TAC CCT AAC CCA GAG  630
N   S   S   C   C   N   R   K   I   I   G   A   R   F   Y   P   N   P   E   206

GAG AAA ACG GCA AGG GAT TTC AAC GGA CAT GGG ACT CAC GTT TCG TCG ACG GCA GTG  687
E   K   T   A   R   D   F   N   G   H   G   T   H   V   S   S   T   A   V   225

GGC GTG CCG GTG AGT GGC GCA TCG TTC TAT GGT CTG GCG GCG GGG ACG GCA AGG GGT  744
G   V   P   V   S   G   A   S   F   Y   G   L   A   A   G   T   A   R   G   244

GGG TCC CCT GAG TCA AGG TTG GCG GTT TAC AAA GTG TGT GGG GCT TTT GGG TCA TGT  801
G   S   P   E   S   R   L   A   V   Y   K   V   C   G   A   F   G   S   C   263

CCT GGG TCG GCC ATT CTT GCG GGG TTT GAC GAT GCC ATT CAC GAC GGA GTG GAT ATC  858
P   G   S   A   I   L   A   G   F   D   D   A   I   H   D   G   V   D   I   282

TTG TCG CTG TCG CTC GGT GGA TTC GGT GGA ACC AAA ACC GAT TTG ACC ACC GAC CCG  915
L   S   L   S   L   G   G   F   G   G   T   K   T   D   L   T   T   D   P   301

ATT GCG ATT GGA GCA TTC CAC TCC GTC CAG CGC GGC ATC CTG GTG GTC TGC GCC GCC  972
I   A   I   G   A   F   H   S   V   Q   R   G   I   L   V   V   C   A   A   320

GGG AAC GAC GGA GAA CCA TTC ACC GTT CTC AAC GAC GCA CCT TGG ATT TTA ACC GTT 1029
G   N   D   G   E   P   F   T   V   L   N   D   A   P   W   I   L   T   V   339

GCA GCT TCC ACC ATC GAC CGT GAT CTT CAA TCC GAC GTG GTC TTG GGT AAT AAC CAA 1086
A   A   S   T   I   D   R   D   L   Q   S   D   V   V   L   G   N   N   Q   358
```

FIG. 23(B)

```
GTC GTC AAG GGA AGA GCC ATA AAT TTC TCC CCT CTT TTA AAT TCT CCC GAT TAT CCA 1143
 V   V   K   G   R   A   I   N   F   S   P   L   L   N   S   P   D   Y   P  377

ATG ATA TAT GCT GAG TCT GCT GCC AGG GCA AAT ATC TCC AAC ATA ACT GAT GCA AGA 1200
 M   I   Y   A   E   S   A   A   R   A   N   I   S   N   I   T   D   A   R  396

CAA TGC CAC CCA GAT TCA TTA GAT CCA AAA AAA GTC ATA GGG AAG ATT GTG GTT TGT 1257
 Q   C   H   P   D   S   L   D   P   K   K   V   I   G   K   I   V   V   C  415

GAT GGA AAA AAT GAC ATT TAT TAT TCA ACT GAT GAG AAA ATT GTC ATA GTG AAG GCG 1314
 D   G   K   N   D   I   Y   Y   S   T   D   E   K   I   V   I   V   K   A  434

TTG GGA GGA ATA GGT CTG GTT CAT ATT ACT GAT CAA TCT GGA TCA GTA GCA TTT TAT 1371
 L   G   G   I   G   L   V   H   I   T   D   Q   S   G   S   V   A   F   Y  453

TAT GTG GAC TTC CCA GTA ACA GAG GTA AAA TCA AAA CAT GGC GAC GCA ATC CTC CAG 1428
 Y   V   D   F   P   V   T   E   V   K   S   K   H   G   D   A   I   L   Q  472

TAC ATC AAC TCA ACT AGC CAT CCA GTG GGA ACA ATA CTA GCA ACA GTT ACA ATT CCT 1485
 Y   I   N   S   T   S   H   P   V   G   T   I   L   A   T   V   T   I   P  491

GAT TAT AAG CCT GCT CCC CGG GTG GGT TAT TTT TCA TCA AGA GGG CCT TCA TTG ATT 1542
 D   Y   K   P   A   P   R   V   G   Y   F   S   S   R   G   P   S   L   I  510

ACA AGC AAT GTT CTC AAG CCT GAT ATT GCA GCC CCG GGA GTT AAC ATT CTC GCT GCA 1599
 T   S   N   V   L   K   P   D   I   A   A   P   G   V   N   I   L   A   A  529

TGG TTT GGA AAT GAC ACA TCA GAG GTT CCA AAA GGA AGA AAG CCC TCA CTA TAT CGC 1656
 W   F   G   N   D   T   S   E   V   P   K   G   R   K   P   S   L   Y   R  548

ATA CTC TCA GGA ACT TCC ATG GCT ACT CCA CAT GTT TCA GGG CTT GCA TGC AGT GTC 1713
 I   L   S   G   T   S   M   A   T   P   H   V   S   G   L   A   C   S   V  567

AAA AGA AAA AAC CCC ACT TGG AGT GCC TCC GCA ATC AAA TCT GCC ATC ATG ACT TCA 1770
 K   R   K   N   P   T   W   S   A   S   A   I   K   S   A   I   M   T   S  586

GCA ATT CAA AAT GAC AAT TTG AAG GGT CCC ATA ACA ACG GAT TCA GGG TTG ATA GCC 1827
 A   I   Q   N   D   N   L   K   G   P   I   T   T   D   S   G   L   I   A  605

ACA CCT TAT GAC TAT GGA GCA GGG GCA ATT ACA ACA TCT GAA CCA TTG CAA CCG GGG 1884
 T   P   Y   D   Y   G   A   G   A   I   T   T   S   E   P   L   Q   P   G  624

CTA GTT TAT GAA ACC AAC AAC GTT GAC TAC TTG AAC TAT TTG TGT TAC AAT GGA CTT 1941
 L   V   Y   E   T   N   N   V   D   Y   L   N   Y   L   C   Y   N   G   L  643

AAC ATA ACC ATG ATA AAG GTC ATC TCC GGA ACT GTC CCC GAG AAT TTC AAT TGT CCC 1998
 N   I   T   M   I   K   V   I   S   G   T   V   P   E   N   F   N   C   P  662

AAG GAT TCG AGC TCT GAT CTC ATC TCC AGC ATC AAC TAC CCT TCC ATA GCA GTA AAC 2055
 K   D   S   S   S   D   L   I   S   S   I   N   Y   P   S   I   A   V   N  681

TTC ACT GGC AAA GCA GAC GCG GTC GTG AGT AGA ACT GTC ACA AAC GTT GAC GAA GAA 2112
 F   T   G   K   A   D   A   V   V   S   R   T   V   T   N   V   D   E   E  700

GAT GAA ACA GTG TAC TTC CCC GTT GTT GAA GCT CCT AGT GAA GTA ATT GTC ACA CTC 2169
 D   E   T   V   Y   F   P   V   V   E   A   P   S   E   V   I   V   T   L  719

TTT CCA TAT AAT CTT GAG TTT ACG ACA AGT ATT AAA AAA CAA AGC TAC AAT ATT ACT 2226
 F   P   Y   N   L   E   F   T   T   S   I   K   K   Q   S   Y   N   I   T  738
```

FIG. 23(B)(Cont'd)

```
TTC AGA CCG AAG ACC TCC TTG AAG AAA GAT TTG TTT GGA TCT ATC ACT TGG AGT AAC 2283
 F   R   P   K   T   S   L   K   K   D   L   F   G   S   I   T   W   S   N  757

GAC AAA TAT ATG GTT CGA ATT CCT TTT GTA TTA ACT AAA TAG tgaaattaaaaagtagcga 2344
 D   K   Y   M   V   R   I   P   F   V   L   T   K   *                      770

tgaataaatgcaagctaagttcttcgtggtgcctacactcgagtcctgattatttattattcatatgccttctgt 2419

tttaatttat ttattatact ttcagcct(a)n                                          2447
```


FIG. 23(B)(Cont'd)

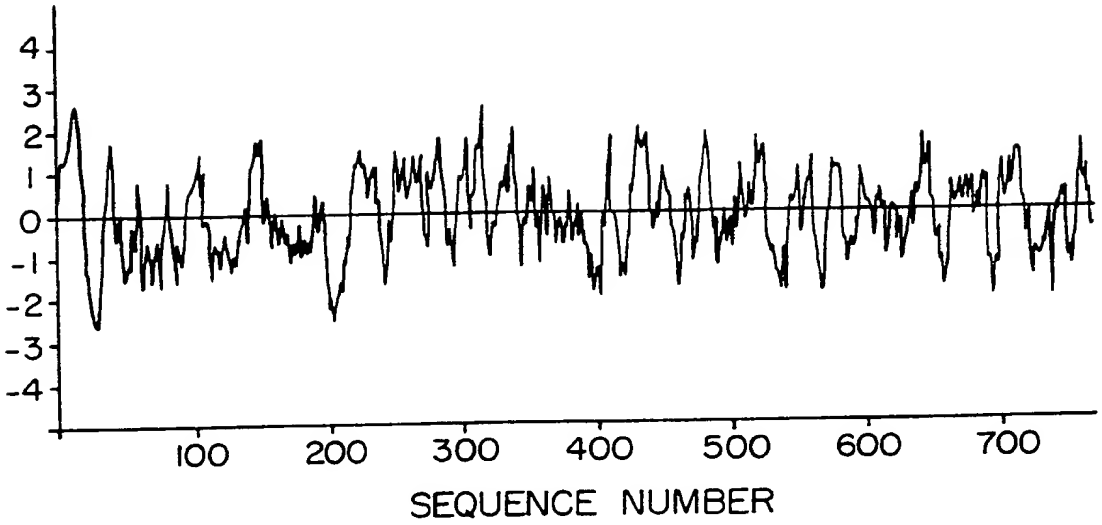


FIG. 23C

D region

SC20:2	SDVILGVLDTGI	156
AF70	TDIILGFLDTGI	145
Cucumisin	SNIVVGVLDTGI	143
P69B	KGVIIGVIDTGI	149
Ag12	EDVIIGVIDSGV	148
Subtilisin BPNÆ	SNVKVAVIDSGI	142
Kex2	AGVVAAIVDDGL	178
Furin	HGIVVSILDDGI	156

H region

SC20:2	DFNGHGTHVSSTAVG	224
AF70	DYQGHGTYTAATAAG	229
Cucumisin	DNTGHGTHTASTAAG	214
P69B	DDIGHGTHTASTAAG	213
Ag12	DTLGHGTHTASTAAG	216
Subtilisin BPNÆ	DNNSHGTHVAGTVAA	181
Kex2	SDDYHGTRCAGEIAA	223
Furin	NDNRHGTRCAGEVAA	204

S region

SC20:2	SGTSMATPHVSGLA	562
AF70	SGTSVAVPHVTGAA	571
Cucumisin	SGTSMSCPHITGIA	535
P69B	SGTSMSCPHLSGVA	541
Ag12	SGTSMACPHASGVA	547
Subtilisin BPNÆ	NGTSMASPHVAGAA	338
Kex2	GGTSAAAPLAAGVY	395
Furin	TGTSASAPLAAGII	378

N region

SC20:2	SVQRGILVVCAAGNDG	322
AF70	ATQKGILVVSSAGNEG	329
Cucumisin	AVERGILTSNSAGNGG	310
P69B	ATERGILVSCSAGNSG	308
Ag12	AMEKGVVVSTSAGNAG	318
Subtilisin BPNÆ	AVASGVVVVAAAGNEG	264
Kex2	RDSKGAIYVFASGNGG	316
Furin	RGGLGSIFVWASGNGG	297

FIG. 23(D)

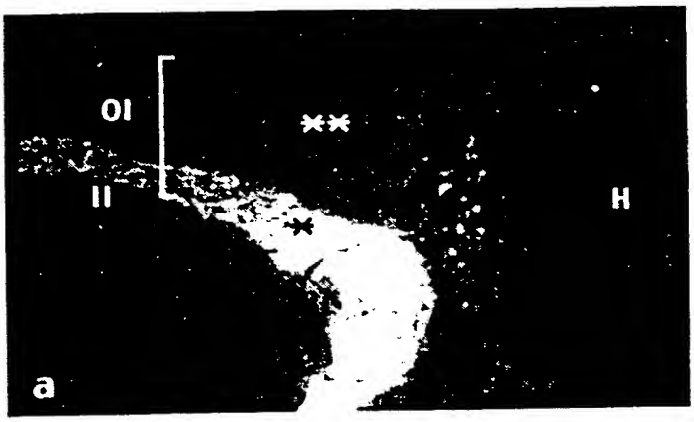


FIG. 24A

FIG. 24B

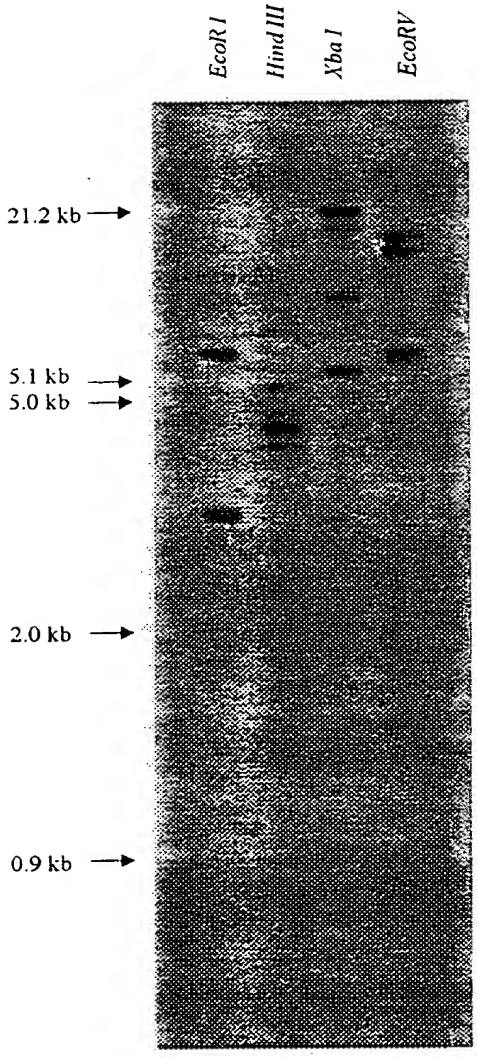
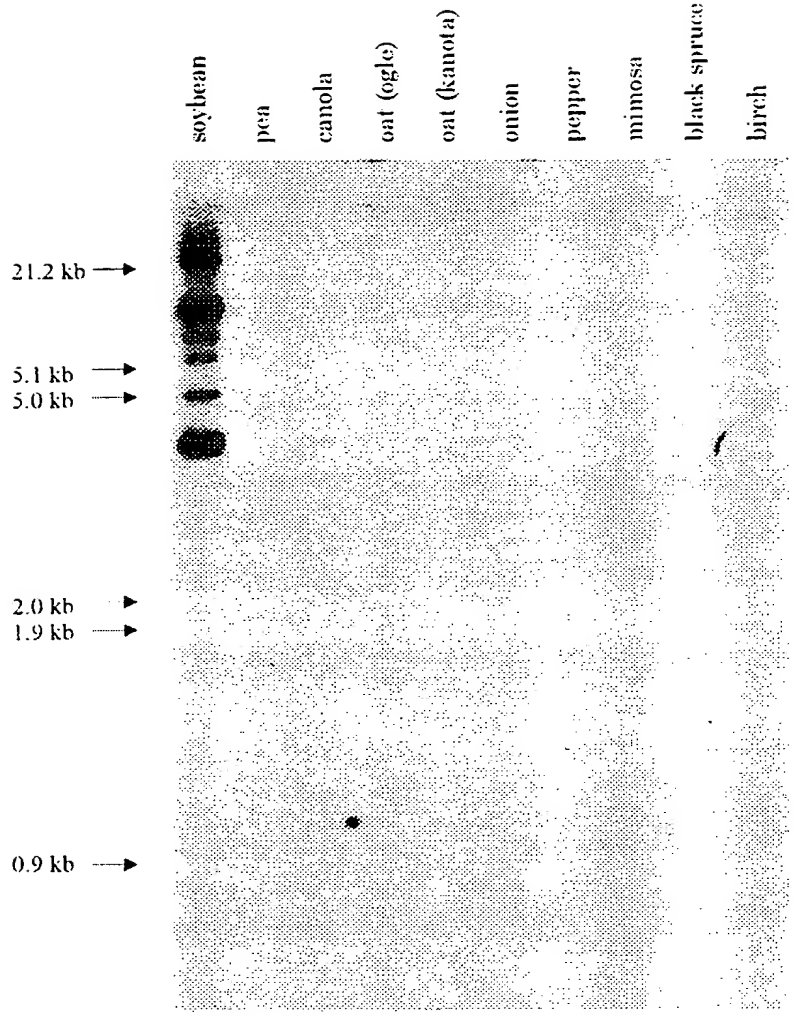


Fig. 25 A

Fig. 25 B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canola
oat (ogle)
oat (kanota)
onion
pepper
mimosa
black spruce
birch
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5.1 kb
5.0 kb
2.0 kb
1.9 kb
0.9 kb

Fig. 25 C